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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                              Result
No.
                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                        1242
864.5
834
768.5
606.5
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                                                                                                                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
      Match
                                                                                                                                                                                                                                                     Query
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   May 27, 2003, 18:25:46; Search time 19 Seconds (without alignments) 1189.031 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                 283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTVLAPAWSPTTYLLLLLLL......RPGEQVPPVPSPQDLLLVEH 235
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1242
                                                                                                                                                                                                                                                                                                                                                 PIR_73:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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pir2:*
pir3:*
pir4:*
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S607201

AB1990

J000257

J000252

A32290

A53137

A4043

A4043

A4043

A33647

A33647

A33647

A33647

A33646

A37374

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A37374

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$43293
139076
A49265
$43291
158343
722672
T198E12
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hypothetical prote
sulfated surface g
hypothetical prote
FC gamma (IGG) rec
tegument protein 6
gamma-glutamyl car
hypothetical prote
transactivator EBN
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
                                                                                                                      Flt3 ligand - huma
FLT3-FLK2 ligand
flt3 ligand altern
flt3/flk 2 ligand
flt3/FLK2 ligand
flt3 ligand isofor
hypothetical prote
74K algha trans-in
hypothetical prote
adhalin - golden h
splicing factor SF
hypothetical prote
hypothetical prote
hypothetical prote
op protein - Kenne
                                                                                               tyrosine kinase re
glutamic acid-rich
                                                                                                              protein-tyrosine-p
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44	442	39 40 10	35 37	ພ ພ ພ 4 ພ ນ	30 31
80.5 80.5	80.5 81	81 82 8	81.5 81.5	82 82 81.5	82.5 82.5
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1176 1306	636 636	. 196 209 294	488 958 1119	106 854 485	512 513
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T49482 T13592	S15591 EHHU JW0047	B48232 A48232 A12016	S13423 T13593 T50995	T06479 T23837 C75460	D40829 JQ1484
9 6 6	probable transposa Ig epsilon chain C class I cytokinasa	<pre>cysteine-rich exte cysteine-rich exte hypothetical prote</pre>	stromelysin 3 (EC) hypothetical prote related to cytoske	/leuc	activin receptor i

ALIGNMENTS

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OY 121 REVOTNISRLLOETSBOLVALKPWITRONESRCLELOCOPDSSTLPPPWSPRPLEATAPT 180	OY 61 ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120	QY 1 MTVLAPAWSPTTYLLLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60 1	Query Match 100.0%; Score 1242; DB 2; Length 235; Best Local Similarity 100.0%; Pred. No. 5.4e-99; Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A;Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-71, 'A',73-235 <han> A;Cross-references: GB:U04806; NID:g483844; PIDN:AAA17999.1; PID:g483845 A;Note: the authors translated the codon AGT for residue 25 as Met C;Genetics: A;Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3</han>	A;Title: Ligand for FLM3/FLK2 receptor tyrosine kinase regulates growth of haematopol A;Reference number: \$43290; MUID:94195428; PMID:8145851 A;Accession: \$43292	A:Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90949.1; PID:g1072037 R;Hannum; C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik Nature 368, 643-648, 1994	A/Status: preliminary; translated from GB/EMBL/DDBJ A/Molecule type: DNA A.Molecule type: DNA	A;Cross-references: EMBL:U03858; NID:g494978; PIDN:AAA19825.1; PID:g494979 R;Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S. Oncogene 11, 1165-1172, 1995	A/Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-235 <res></res>	murine flt3 l D:8180375	C.Spectes: Homo sapiens (man) C.Spectes: 19-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000 C.Accession: I38440; I39075; S43292 C.Accession: I38440; I39075; S43292 R.Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe	RESULT 1 I38440 flt3 ligand - human	

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Q
                                                                                                                                               C;Genetics:
A;Introns: 11/3; 48/3;
                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-178 < RES>
                                                                                                                                                                                                                                                            C;Accession: I39076

R;Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Oncogene 11, 1165-1172, 1995

A;Title: Structural analysis of human and murine fit3 ligand genomic A;Reference number: I39075; MUID:96032581; PMID:7566977

A;Accession: I39076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S43293
R; Hannum, C.; Culpepper, Cfelt, A.; Muench, M.; Kelr
Nature 368, 643-648, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
$43293
FLT3/FLK2 ligand (clone S109)
C;Species: Homo sapiens (man)
C;Date: 20-Oct.1994 #sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoiet A;Reference number: $43290; MUID:94195428; PMID:8145851
A;Accession: $43293
A;Status: preliminary
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                                                                                                                                                                                 Cross-references: EMBL:U29874; NID:g1072036; PIDN:AAA90950.1;
                                                                                                                                                                                                                                                                                                                                                                      ;Species: Homo sapiens (man)
;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
                                                                                                            Query Match
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APQP-----PLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTVLAPAWSPTTYLLLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncaro
                               MTVLAPAWSPTTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPGA---PRPQSPGPAACGALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH
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160;
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                                                                                        Similarity
                                                                      ilarity 100.0%;
Conservative 0;
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                                                                                                                                               66/3; 114/3; 161/1
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73.08;
                                                                   67.1%; Score 834; DE 100.0%; Pred. No. 3.3 tive 0; Mismatches
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Pred. No. 1.2e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----ARGCIAWTORKLARGRSLPWAPLIPSP
                                                                                                                                                                                                                                            GB/EMBL/DDB.
                                                                                      3.3e-64;
                                                                                                          DB 2;
                                                                                                        Length 178
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                                                                    Indels
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Roncarolo, M.G.; Zlotnik,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
                                                                                                                                                                               PID:g1072038
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Best Local Similarity
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                                                                                    120
                                                                                                                          61
                                                                                                                                                               60
                                                                    LRFVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPRPLEAT 177
                                                                                                                                                                                                                    MTVLAPAWSP-TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVT
       APTAPQPP---LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP
                                               LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPDSSTLLPPRSPIALEAT
                                                                                                                        VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                           VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                               MTVLAPAWSPNSSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                              163;
                                                                                                                                                                                                                                                                            Conservative
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RESULT 4
A49265
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: A49265; I49347; I49346; S43290
C;Accession: A49265; I49347; I49346; S43290
                                                                                                                                                                                    A:Molecule Type: mRNA, A:Residues: I-197, L; 198-231 <HAN> A:Residues: I-197, L; 198-231 <HAN> A:Experimental source: clone T110 A:Note: the sequence from Fig. 2c is inconsistent with C:Genetics: A:Introns: 11/3: 49/3: 67/3: 115/3: 164/1: 224/3 C:Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040 R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazz felt, A.; Muench, M.; Kelner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Nature 368, 643-648, 1994
A:Title: Vicens 6 Common Commo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates A;Reference number: S43290; MUID:94195428; PMID:8145851 A;Accession: S43290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L23636; NID:g439441; PIDN:AAA39436.1; PID:g439442 R;Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Esc. Oncogene 11, 1165-1172, 1995 Pittle: Structural analysis of human and murine flt3 ligand genomic loc A;Reference number: I39075; MUID:96032581; PMID:7566977 A;Accession: I49347
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A;Reference number: A49265; MUID:94084791; PMID:7505204
A;Accession: A49265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Lyman, S.D.; James, L.; Vanden Bos, T.;
D.; Williams, D.E.; Beckmann, M.P.
Cell 75, 1157-1167, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-197, 'L', 198-231 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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61.9%; Score 768.5; DB: 70.3%; Pred. No. 1.8e-58 tive 17; Mismatches 4:
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A;Title: Identification of soluble and membrane-bound A;Reference number: I58343; MUID:95124710; PMID:782426
                 밁
                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-220 <RES>
A;Cross-references: GB:S76459; NID:g913479; PIDN:AAB33069.1;
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A;Accession: S43291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: S43291
R; Hannum, C.; Culpe
felt, A.; Muench, M
                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A;Accession: I58343
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Date:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Hannum, C.; Culpepper, J.; Campbell, felt, A.; Muench, M.; Kelner, G.; Nami. Nature 368, 643-648, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  flt3 ligand isoform 5H -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule
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$43291
FLT3/FLK2 ligand (clone Tl18) - mouse
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                                                                                                                                                                                                                                               Query
                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: I58343
                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Mus sp. (mouse)
Date: 26-Jul-1996 #sequence_revision
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                                                                                                                                                       MTVLAPAWSP-TTYLLLLLLLSGLSGTQDCSFOHSDISSDFAVKIRELSDYLLQDYPVT
                                     LREVOINISRLLQEISEQLVALKPWITR - - QNFSRCLELQCQPDSSILPPPWSPRP - - - -
                                                                      VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                         VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                       MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
          LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLEVQCQPGNG---
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1-220 <HA
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                                                                                                                                                                                                           Score 606.5;
Pred. No. 1.3e
.8; Mismatches
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Pred. No. 1.:
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, R.; Rennic
                                                                                                                                                                                                                            1.3e-44;
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1.3e-44;
es
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Rennick, D.; Roncarolo, M.G.; Zlotnik,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212
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C;Superfamily: herpesvirus 77K alpha trans-inducing protein
C;Keywords: trans-inducing protein; transcription regulation
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C;Date: 15-Oc
C;Accession:
                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-661 <DAV>
                                                                                                                                                                                                                                                                                                                                                                    R;Davison, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
                                                                                                                                                                                                                                                                                                                                                                                                 74K alpha trans-inducing protein - human herpesvirus 3
C;Species: human herpesvirus 3, varicella-zoster virus
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
C;Accession: C27342
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submitted to the EMBL Data Library,
a.Reference number: Z19597
                                                                                                                                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                                                                                                                                                       A; Accession: C27342
                                                                                                                                                                                                                                                                                                                                     A; Reference number:
                                                                                                                                                                                                                                                                                                                                                    A; Title: The complete
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A; Introns: 742/2; 826/1;
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A; Residues: 1-1217 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:281548; NID:e1062020; A;Experimental source: clone F54F12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from
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                                                                                                                                      Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Caenorhabditis elegans;Date: 15-Oct-1999 #sequence_revision;Accession: T22672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         local Similarity
                                                                                            LLSSGISGTQDCS----FQHSPISSDFAVKI--RELSDYLLQDYPVTVASNLQDEELCG- 71
GLW-WVYENTYWQYLKYTTGAEVPVTSEKVNKKSKSTVLLFSSVVANKPISRHPFKSKVI
                             GLWRLVLAQRWMERLKTVAGSKMQGLLERVN----TEIHFVTKCAFQP---PPSCLRFV 123
                                                               LTSPVLQSTERHSVLLGLHHNNVPESLVVSCMSNDVHDGFMQRYMETIQRCLDDLKLSGD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALKPWITRONFSRCLELOCOPDSSTL---PPPWSPRPLEATAPTAP----OPPLLLLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDAVKAVDGTKYSSVIDALEKLSTMDLDFQKYKFKEAPATLKAMDL----FFASYASNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAVGGLLVVAIIGVILFFVFFQKKKKKEDKPDD--PPAPLP
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                                                                                                                                                    Similarity
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                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                   te DNA sequence of varicella-zoster A27345; MUID:86306657; PMID:3018124
                                                                                                                                                                                                                                                                  EMBL: x04370; NID: g59989;
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                                                                                                                                                    7.48;
26.68;
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                                                                                                                                                Score 92;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 93; DB 2
Pred. No. 8;
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      November
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                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                  PIDN:CAA27895.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIDN:CAB04464.1;
                                                                                                                                 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68;
                                                                                                                                                                 Length 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      781
                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                  PID:960001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSPDB:GN00021;
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     682
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6

CESP:F

11;

Gaps

14;

--------EVPTPGD 266

204

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C;Species: Caenorhabditis elegans
C;Date: 15-Cct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19543
                                                          A;Cross-releasement. _____C;Superfamily: mouse adhalin
                                                                                                                                                                                                                                                                      C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000
C;Accession: I48201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, A; Reference number: Z19139
A; Accession: T19543
                                                                                                                                                   A;Title: Adhalin mRNA and cDNA sequence are normal in the A;Reference number: I48201; MUID:95278335; PMID:7758576 A;Accession: I48201
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                               R;Roberds, S.L.; Campbell, K.P. FEBS Lett. 364, 245-249, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 4
A; Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                                                                                                                                                                                                                                                                                            adhalin – golden hamster
                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;McMurray,
                                                                                  Molecule type: mRNA
Residues: 1-387 <RES
Cross-references: EMBL:U21677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA
Residues: 1-474 <WIL>
                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Experimental source: clone C28D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: EMBL: 282259; PIDN: CABO5129.1; GSPDB: GN00022; CESP: C28D4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated from GB/EMBL/DDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene: CESP:C28D4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179
                                                                                                                                                                                                                                                                                                                                                                                                                               267
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Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 GYGWMLWFLDVVD-----ARVCRHLKLQFRRIRGPRASV----IPDDLL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLVE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKIEEF -- RIRAITGG-MSNLLFLVELPAH-LTPIQMEPEKALLRVHCQSDIDQLLSESV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLR-FVQTNÍSRLLQET- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQDC------SFQHS-PISSDFAVKIREL-SDYLLQDYPVTVASNLQDEELCGGLWRL 76
                                                                                                                                                                                                                                                                                                                                                                                                                             ITVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKEPQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTAPQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTP---RPGE-----QVPPVPSPQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFTLLSERNLGPKMLGVFPGGRFEQFIPSRALQCLEISKPGLSKLIAPIVARVHTLDAPI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SEQLVALKPWITRQNFSRCLELQC----QPDSSTLPPPWSPR--PLEATA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPPLLLLLLPVGLLLLAAAWCLHWQRTRRTPRPGEQVPPVPSPQDLL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSDYRGICQELREALGAVQKYM---YFMR-----PDDPTNPSPDTRIRVQEIAAYTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P
                                                                                                                                                                                                                                                                                                                                                                                                                             271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.2%; Score 89.5; D
24.1%; Pred. No. 5.5;
                7.2%;
23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLQTARQWLERF----KKEPAGERPIEMYLTQAKVPKSDYPST 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                          NID: g726481; PIDN: AAA81645.1;
              Score 89;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                DB 2;
4.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82;
                                  Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                         cardiomyopathic hamster.
                                                                                          PID: g726482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross references: GDB:9955873
A;Map position: 22q12.1-22qter
C;Superfamily: human splicing factor SF3a 120K chain; ubiquitin C;Keywords: pre-mRNA splicing
F;714-790/Domain: ubiquitin homology <UBH>
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C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C:Accession: S60735; S60733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X85237; NID:g899297; PIDN:CAA59494.1; PID:g899298
A;Accession: S60733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB:SF3A120; PRP21; SAP114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 51-62;82-94;270-275;397-414;448-463 <KRA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: S60735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Mammalian splicing factor SF3a120 represents a A; Reference number: S60733; MUID:96079958; PMID:7489498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splicing factor SF3a 120K chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Kraemer, A.; Mulhauser, F.; Wersig, C.; Groening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
Residues: 1-793 <KRA>
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                537
                                                                                                                                                                                                                                                                  401
                                                                                                      479 VEETAIGKKIGEEEIQKPEEKVTWDGHSGSMARTQQAAQANIT--LQEQIEAIHKAKGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 LDQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 LVEH 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 MATSDIQMVHHCTIHGNTEELRQMAARREVPRPLSTLPMFNVRTGERLPPRVDSAQVPLI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 GILEHDPFFCPPTEATGRDFLADALVTLLVPLLVALLL---TLLLAYIMCCRREGQLKRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 SSTLPPPWSPRPLEAT-----APTAPOPPLLLLLLPVGLLLLAAAWC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 CAFQPPP--SC-----LRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 GGLWELGELQLLNITSALDRGGRVPLPIEGRKEGVYIKVGSATPFSTCLKMVASPDSYAR 221
                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260-272,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                    4 LAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63
                            PEDDTKEKIGPSKPNEIPQQPPPPSSATNIPSSAPPITSVPRPPTMPPPVRTTVVSAVPV
                                                                  ----TRONF--SRCLELQCQP----
                                                                                                                                               VTKCA-----FQPPPSCLRF---
                                                                                                                                                                                   MQEHMRIG-----LLDPRWLEQRDRSIREKQSDDEVYAPGLDIESSLKQLAER-RTDIFG
                                                                                                                                                                                                                         LQDEELCGGLWRLVLAQRWME-RLKTV------
                                                                                                                                                                                                                                                                  LPPAPAPDEYLV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAQGQPPLLSCYDSLAPHFRVDWCNVSLVDKSVPEPLD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGLWRL-----VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTRORLLLII-----EDPEGPRLPYQAEFLVRSHDVEEVL----PSTPANRFL--TAL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC 70
                                                                                                                                                                                                                                                                                                                                          67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                            22.3%;
                                                                                                                                                                                                                                                                                                                                                            7.2%; Score 89; 22.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                        ; Pred. No. 11; 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                                -----SPITGE---KI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                  -DSSTLP-----PPWSPRPLEAT----APT 180
                                                                                                                                             -----VQTNISRLLQETSEQLVALKPWI 145
                                                                                                                                                                                                                                                                                                                                                            DB
11;
                                                                                                                                                                                                                                                                                                                                                                            1.
                                                                                                                                                                                                                                                                                                                                          79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97;
                                                                                                                                                                                                                       -AGSKMQGLLERVNTEIHF 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                          Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 110;
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<u>ດ</u>

of the

SURP family

----PASK 424

536

478

Gaps

17;

homology

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A; Experimental source: brain C; Genetics: A; Note: KIAA0476
                                                                                                                                                                                                                                                                       R;Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; DNA Res. 4, 345-349, 1997
A;Title: Characterization of cDNA clones in size-fractionated cDNA libraries A;Reference number: Z14085; MUID:98116662; PMID:9455484
A;Accession: T00257
            밁
                                             Ş
                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-1386 <SEK>
                                                                                                                                                                                                                                                                                                                                                                 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change Aj-Jul-2000
C:Accession: T00257
                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein KIAA0476 - C; Species: Homo saniene 'men'
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A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Note: Nostoc sp. strain PCC 7120 is a synonym of C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 C:Accession: AB1990
                                                                                                                                                                                                                                                     A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-238 <KUR>
A; Cross-references: GB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein all1471 [imported] - Nostoc
                                                                                                Query Match
Best Local :
                                                                                                                                                                                                    Cross-references: EMBL:AB007945;
                                                                                                                                                                                                                                                                                                                                                                Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Nostoc sp.
            1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 GLLLLAAAWCLHWORTRRRTPRPGEQVPPVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132
                                      21 SSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYTVASNLQDEELC----GGLWRL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 APOPPLLLLLLLPVGLLLLAAAWCLHWQRTR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
          SAGASGSKDAPVPGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVALKPWITRONESRCLELOCOPDSSTLPPPW---SPRPLEATAPTAPOPPLLLLLLLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQ------ETSEQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPRPPMASVVRLPPGSVIAPMPPIIHAPRINVVPMPPSAPPIMAPRPPPMIVPTAFVPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSKKTTTYYESINEVCNQYLKSYEKKPLVII-----QILG--W----SQRLMRYYKTVD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TKPIPPKLIEPKKSEDSKNLQRPRIPDSPKPIKNSQPEAPKPV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB:BA000019; F
                                                                                              7.18;
23.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -EPPKPWERVPKKPS
                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                   Score 88.5; pred. No. 23; 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIDN:BAB77837.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 88.5; D
Pred. No. 3;
32; Mismatches
                                                                                                                                                                                                                                                      from
                                                                                                                                                                                                  NID: g3413913;
     -GPVLSDRRLCLA--LDEPQLCNGHMGGASRR 1148
                                                                                                                                                                                                                                                     GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -VVRKIPKVIETPKIVKPQKTEDIKTLES
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                                                                                                                                                                                                PIDN:BAA32321.1;
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                                                                            85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anabaena sp. strain PCC 
#text_change 30-Jun-2002
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                                                                                                            Length
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                                                                            Indels
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                                                                                                                                                                                                                                                                                                      cDNA libraries from human
                                                                          63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77;
                                                                                                                                                                                              PID: 93413914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watanabe,
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                                                                      Gaps
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                                                                                                                                                                                          R;Edgar, B.A.; O'Farrell, P.H.
Cell 57, 177-187, 1989
A;Title: Genetic control of cell division patterns in the A;Reference number: A32290; MOID:89195217; PMID:2702688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
JQ0532
OP protein
                                                                                                                                                                                                                                                                                protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25 homolog C;Species: Drosophila melanogaster C;Date: 05-Cct-1989 #sequence_revision 25-Apr-1997 #text_C;Accession: A32290; S12008
                                                                    A; Title: Complementation of fission yeast cdc2(ts) and A; Reference number: S12008; MUID:91006056; PMID:2120044
                                                                                                         R; Jimenez, J.; Alphey, L.; Nurse, EMBO J. 9, 3565-3571, 1990
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A;Residues: 1-227,'A',229-479 <JIM>
A;Cross-references: EMBL:X57495; NI
                                  A; Molecule type: mRNA
                                                    A; Accession: S12008
                                                                                                                     A;Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; R;Jimenez, J.; Alphey, L.; Nurse, P.; Glover, D.M.
                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-479 <EDG>
                                                                                                                                                                                                                                                                                                                                                       A32290
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NID: 97706; PIDN: CAA40732.1;

PID: 97707

cdc25(ts)

mutants

identifies

PID: g158508

25-Apr-1997 #text_change

11-Jun-1999

Drosophila embryo

string

fruit fly

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A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-753 <DIN>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The nucleotide sequence of the genomic RNA of A;Reference number: JQ0532; MUID:90218040; PMID:2324710 A;Accession: JQ0532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Ding, S.; Keese, P.; Gibbs, A.
J. Gen. Virol. 71, 925-931, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OP protein - Kennedya yellow mosaic virus
C;Species: Kennedya yellow mosaic virus
C;Date: 31-Dec_1993 *sequence_revision 31-Dec-1993 *text_change 28-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: JQ053
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1254 LYVL---
                                                                                                                                                                                                                                                                                                                  100 RVNTEIHFVTKCAFQPPPSCLRF----VQTNIS-----RLLQETSEQLVALKPWITR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 LLLLLLPYGLLLLAAAWCLHWQRTRRTPRPGEQVPPVPSPQDLLLVE
                                                                                       PPDVFHDCQPSSPTSHVVGYRRLLGSGISLPFKLAFW----
                                                                                                                                                                                                                                                                         RLSTQPPSSPQTSSSPPPPSPRTDASGIQTPLASPPSKRKEKSLPHPSHQ----PPSHSK 475
PRKL
                                           PODL
                                                                                                                                                                               RNLRRHSALPLLLPIHPTKTTQPHPAVPQP--TAGPTPHPPPTKKIPLHPPKSQERHPSP 533
                                                                                                                                                                                                                             QNFSR----CLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VESGAWAYLSPLVLRKELESLVENEGSEV-----LALPELPSAHPIIFWNLLWYFQRL--
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                                                                                                                                                                                                                                                                                                                                                                          41;
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:D00637; NID:g221969; PIDN:BAA00531.1; PID:d1000986; ce: strain Jervis Bay isolate
                                                                                                                                                                                                                                                                                                                                                                                           7.1%;
22.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -WRVHSQ-IPQRVVWPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- CDGPSHSQAPSPWLTPDPASVQVRLLWDVLTPDPNSCPP
                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                              Score 88; DB Pred. No. 12;
                                                                                                                                -VGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPS 226
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -PVPASLSLALLE
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                                                                                                                                                                                                                                                                                                                                                                     58;
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 753
                                                                                       RRRSPNPARHLPPPPP
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kennedya
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                                                                                                                                                                                                                                                                                                                                                                   66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yellow mosaic tymovir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID: g22197
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C:Genetics:
A:Gene: FlyBase:stg
A:Cross-references: FlyBase:FBgn0003525
Search completed: May 27, 2003, 18:27:59 Job time: 22 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match. 7.0%; score 87.5; b
Best Local Similarity 22.9%; Pred. No. 8.2;
Matches 56; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pathway: initiation of mitosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    te: cdc25 activates the cdc2 protein kinase by dephosphorylating it perfamily: protein-tyrosine-phosphat perfamily: protein-tyrosine-phosphatase string; cdc25-type protein-tyrosine-phosphat ywords: cell cycle control; mitosis; phosphoprotein; phosphoric monoester hydrolase; 2-456/Domain; cdc25-type protein-tyrosine-phosphatase homology <PTP>
9/Active site: Cys (phosphocysteine intermediate) *status predicted
                                                                                                                    243 VTISH 247
                                                                                                                                                                            231 LLVEH 235
                                                                                                                                                                                                                                200 ---TARDCFKRPEPP---
                                                                                                                                                                                                                                                                              174 LEATAPTA:---POPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDL 230
                                                                                                                                                                                                                                                                                                                                              147 SGLN-----SLISGQIKEQPAAKSPAGLSMRRPSVRRCLSMTESNTNSTTTPPPKTPE- 199
                                                                                                                                                                                                                                                                                                                                                                                                                     118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 VTVASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MTVLAPAWSPTTYLLL---LLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYP 57
                                                                                                                                                                                                                                                                                                                                                                                                   SCLREVQTNISRLLQETSEQLVALKP---WITRQNFSRCLEL-QCQPDSSTLPPPWSPRP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGLLSPEGSPORFOIVROPKILPAMGVSS-----DHTPARS-FRI-FNSLSS-----T 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     substrate phosphate (Arg)
                                                                                                                                                                                                                          ----ASANCSPIQSKRHRCATVEKENCPAPSPLSQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 479;
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Title:
Perfect s
Sequence:
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Maximum
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Maximum Match 100%
Listing first 45 s
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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SSGP_VOLCA
ATF5_MOUSE
SGCA_MOUSE
EPC_HUMAN
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IF4G_RABIT
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P29178 hepatitis b	Q92794 homo sapien	P43098 c fatty aci	Q9kqh4 vibrio chol	Q01755 mus musculu	Q55854 synechocyst		Q08345 h epithelia		P38445 rattus norv	P17483 homo sapien	P53086 saccharomyc

ALIGNMENTS

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a collaboration

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RESULT 2
FLJL_MOUSE
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Matches 235
                                                                                  FL3L_MOUSE STANDARD; PRT; 232 AA. P49772; Q64085; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) SL cytokine precursor (Fms-related tyrosine k ligand) (Fl13L).
SEQUENCE FROM N.A. MEDLINE-94195428;
                                          Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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CONFLICT
SEQUENCE
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VARSPLIC
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EMBL; U29874; AAA90949.1; --
EMBL; U29874; AAA90950.1; --
EMBL; U29874; AAA90950.1; --
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use by non-profit institutions as its content is in no way
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch):
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 PubMed=8145851;
                                          Chordata;
Rodentia;
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MISSING (IN ISOFORM 2).
G -> A (IN REF. 1).
73B95BF693B4CECF CRC64;
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CYTOPLASMIC
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EXTRACELLULAR (POTENTIAL).
                                         Craniata; Ver
Sciurognathi;
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Pred. No. 1.1e-96;
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REAL PROPERTY OF THE PROPERTY 
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EMBL; L23636; AAA39436.1; --
EMBL; U29875; AAA90951.1; --
EMBL; U29875; AAA90952.1; --
EMBL; S76459; AAB33069.1; --
EMBL; S76461; AAB33070.1; --
EMBL; S76461; AAB33071.1; --
EMBL; S76461; AAB33071.1; --
EMBL; U44024; AAA93307.1; --
EMBL; U44024; AAA93306.1; --
EMBL; U44024; AABB; --
EMBL; U44024; AAA93306.1; --
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or send an email t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification of soluble and membra flt3 ligand generated by alternative oncogene 10:149-157(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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MEDLINE=94084791;
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Escobar S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FACTORS AND INTERLEUKINS.
SUBUNIT: Homodiner (soluble isoform) (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein. Two soluble isoforms are also produced by alternative splicing. One of isoform 3/E6, is biologically active, while the other, isof 4/E6Delta16, is inactive.

ALTERNATIVE PRODUCTS: 4 isoforms; 1/6C (shown here), 2/5H, and 4/E6Delta16; are produced by alternative splicing.
                              Pro; IPR004213; PF02947; flt3_:
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11:1165-1172(1995).
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M.P., Copeland
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Transmembrane;

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or send a
                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1989
01-MAR-1989
01-NOV-1990
                                                                                                                                                                           "The complete DNA sequence of varicella-zoster virus.";
J. Gen. Virol. 67:1759-1816(1986).
-i- FUNCTION: MODULATE ALPHA TRANS-INDUCING FACTOR-DEPE
ACTIVATION OF ALPHA GENES.
                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Alphaherpesvirinae; Varicellovirus. NCBI_TaxID=10338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATI2_VZVD
P09264;
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                                     requires a license agreement (See http:
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70.0%;
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Pred. No. 3.6e-57;
7; Mismatches 43
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SL CYTOKINE.
EXTRACELLULAR
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MISSING (IN REF. 2)
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VOCOP -> GLIMQARLTLNSKOSSCLSVLSAGIT
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--LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

DSSTLLPPRSPIALEATELPEPRPRQLLLLLLLLLLLPLTLVL
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LAAAWGLEWORARREGELHPOYPLPSHP -> GNGGPRACH
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                              FACTOR-DEPENDENT
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GBR2_HUMAN STANDAKU;
GBR2_HUMAN STANDAKU;
GBR2_HUMAN STANDAKU;
GBR2_HUMAN STANDAKU;
GBR2_HUMAN STANDAKU;
GFR2_HUMAN STANDAKU;
GFR2_HUMAN STANDAKU;
GCGT-2001 (Rel. 40, Cast sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gamma-aminobutyric acid type B receptor, subunit 2 precursor (Gamma-aminobutyric acid type B receptor)
                                          TISSUE-Hippocampus;
Borowsky B., Laz T.
Submitted (JAN-1999
                                                                                                                                                                  "Cloning and characterization of a novel human with high affinity for GABA and low affinity for Submitted (NOV-1998) to the EMBL/GenBank/DDBJ d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            Herzog H.;
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                MEDLINE=20193514; PubMed=10727622; Clark J.A., Mezey E., Lam A.S., Bonner "Distribution of the GABA(B) receptor sprain Res. 860:41-52(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GABA(B) receptor.";
Nature 396:679-682(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White J.H., Wise A., Main M.J., Gre Barnes A.A., Emson P., Foord S.M., I "Heterodimerization is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Cerebellum;
MEDLINE-99087321; PubMed-9872316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR005051; Herpes_UL46.
Pfam; PF03387; Herpes_UL46; 1.
Transcription regulation; Trans-acting
SEQUENCE 661 AA; 74272 MM; C5CA77A1
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PIR; C27342; TNBE12.
                                                                                                                                                                                                                                                                           Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE FROM N.A.
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                                          3., Laz T.,
(JAN-1999)
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McCrea K., Watson
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                                                                                                                   (ISOFORM 2A).
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C5CA77A16D365379 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Green A., Fraser N.J., M., Marshall F.H.; for the formation of a
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T. Pharmacol. Exp. Ther. 293:460-467(2000).

C. -- FUNCTION: RECEPTOR FOR GABA. THE ACTIVATY OF THIS RECEPTOR IS:
C. -- FUNCTION: RECEPTOR FOR GABA. THE ACTIVATY OF THIS RECEPTOR IS:
C. -- FUNCTION: RECEPTOR FOR GABA. THE ACTIVATY OF THIS RECEPTOR IS:
C. -- FUNCTION: SET OF THE ACTIVATES POTASSIM CHANNELS;
C. STIMULATES PHOSPHOLIFASE A2, ACTIVATES POTASSIM CHANNELS AND MODULATES:
C. INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES:
C. INACTIVATES OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
C. GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
C. GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
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C. GABA-B-R DECREASE NEURONAPTIC POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
C. GABA-B-R DECREASE NEURONAL EXCITABILITY.
C. GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
C. GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
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C. GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATION AND
C. SYNAPTIC INHIBITION BOTALSO IN HIPPOCAMPAL LONG-TERM
C. SYNAPTIC INHIBITION BOTALSO IN HIPPOCAMPAL LONG-TERM
C. ANTINCCLORATION AND BANCE SLEEP, MUSCLE RELAXATION AND
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Sullivan R., Chateauneuf A., Coulombe N., Kolakowski L.F. Jr.,
Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,
Abramovitz M., O'Neill G.P., Ng G.Y.K.;
"Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))
receptors with truncated receptors and metabotropic glutamate
receptor 4 supports the GABA(B) heterodimer as the functional
receptor.";
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"Identification of a GABAB receptor subunit, gb2, required for functional GABAB receptor activity.";
J. Biol. Chem. 274:7607-7610(1999).
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Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan Kargman S., Chateauneuf A., Tsukamoto N., McDonald T., Whiting P., Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression GABABR1.";
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"Molecular identification of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 56:288-295(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rla-R2 INTERACTION
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Chateauneuf A., Cou
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ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2A (SHOWN HERE), 2B AND 2C; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN CEREBRAL CORTEX, THALAMUS, HIPPOCRAMPUS, FRONTAL, OCCIPITAL AND TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, ANYGDALA AND MEDULLA. WEAKLY EXPRESSED IN HEART, TESTIS AND SELETAL MUSCLE.

DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION WEDDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.

SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HETERODIMER OF IS EFFECTIVE ON ITS OWN
                                                                                                                                                                                                                                                                                                                                                                            PREREQUISITE FOR PLASMA MEMBRANE.
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nald T., Bonnert T., F
Coulombe N., Kargman
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ey T., Evans
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pfam; PE01094; ANF_Teceptor; 1.

PROSITE; PS00979; G_PROTEIN_RECEP_F3_1;

PROSITE; PS00980; G_PROTEIN_RECEP_F3_2;

PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;

PROSITE; PS00259; G_PROTEIN_RECEP_F3_3;

PROSITE; PS50259; G_PROTEIN_RECEP_F3_3;

PROSITE; PS00250; G_PROTEIN_RECEP_F3_3;
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; FALSE_NEG.
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SEQUENCE
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FEBS Lett
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"Both hypertrophic and dilated cardiomyopathies are caus of the same gene, delta-sarcoglycan, in hamster: an anin disrupted dystrophin-associated glycoprotein complex."; proc. Natl. Acad. Sci. U.S.A. 94:13873-13878(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
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STRAIN-F1B; TISSUE-Skeletal muscle;
MEDLINE-95278335; PubMed-7758576;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Syrian; TISSUE-Heart muscle; MEDLINE-98054328; PubMed-9391120;
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                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX. SUBCELLULAR LOCATION: Type I membrane protein. Sar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKELETAL
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                   GGLWRL----
                                                                                                  TTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELC
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                                                              TTRQRLLLLI - -
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                                                                                                                                         h 7.2%;
Similarity 23.4%;
71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-profit institutions as long and this statement is not removed
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coglycan precursor (Alpha-SG) (Adhalin)
glycoprotein) (50DAG).
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Pred. No. 2.6;
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EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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Sciurognathi; Muridae; Cricetinae;
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RX MEDLINE-20057165; PubMed-10591208;
RX MEDLINE-20057165; PubMed-10591208;
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Clamp M., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clamp D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Concoy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Chami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Hail R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hail R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Martyn I.D., Mashreghl-Mohammadi M., Matthews L.H., McCann O.T.,
RA McClay J., McLaren S., McMurray A.A., Milnes S.A., Mortimore B.J.,
RA McClay J., McLaren S., McMurray A.A., Milnes S.A., Mortimore B.J.,
RA McClay J., McLaren S., McMurray A.N., Milnes S.A., Mortimore B.J.,
RA Williams L., Hulmb R.W., Stace C.D., Smalley S., Smith M.L.,
RA Williams L., Hulmb R.W., Stace C.D., Smalley S., Smith M.L.,
RA Williams L., Hulm R.K., Skuce C.D., Smalley S., Smith M.L.,
RA Williams L., Hulm R.K., Skuce C.D., Shalley S., Smith M.L.,
RA Williams S.A., Williams S.A., Williams T. E., Wilming L.,
RA Williams S.A., Lin S.-P., Loh P., Beck S., Rogers J., Shimizu N.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Phan S., Cathy S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Mang Q., Wang Y., Wang Y.
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01-NOV-1997
15-JUN-2002
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"Mammalian splicing factor SF3al20 represents
SURP family of proteins and is homologous to t
factor PRP21p of Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-96079958; PubMed-7489498;
Kraemer A., Mulhauser F., Wersig C.,
"Manmalian splicing factor SF3al20 r.
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SF3A1 OR SAP114.
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Q15459;
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Metazoa; Primates;
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35, Last sequence update)
41, Last annotation update)
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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ts a new member
o the essential
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Homo.
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                                                                                                               H.I.,
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Best Local (
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EMBL; AC004997;
HSSP; Q15843; IN
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Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K., Nelson J.,
Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
Emanuel B.S., Shakh T., Kurahashi H., Saitta S., Buddarf M.L.,
McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.
Sgroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
Ullinson D. Dedanteich A. Marting W. U., Vebra A. G. 150.
                                                                                                                                                                                                                                            DOMAIN
DOMAIN
NIAMOD
                                                                                                                                  SEQUENCE
                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000061; Surp.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
Pfam; PF01805; Surp; 2.
SMART; SM00213; UBQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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[3]
                                                                                                                                                                                                                     DOMAIN
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Tilahun Y., Wright
                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Das R., Zhou Z., Reed R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20337962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Functional association
4 LAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF US NRNP TO BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA, SEQUENCE INDEPENDENT BINDING OF SF3A/SE3B COMPLEX UPSTREAM OF THE BRANCH SITE IS ESSENTIAL, IT MAY ANCHOR UZ SNRNP TO THE PRE-MRNA, MAY ALSO B INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.

SUBUNIT: COMPONENT OF SPLICING FACTOR SF3B WHICH IS COMPOSED THREE SUBUNITS; SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP114. SF3A ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TEORM THE UZ SMALL NUCLEAR RIBONUCLEOPROTEINS COMPLEX (UZ SNRN THE UZ SMALL NUCLEAR RIBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTS WITH SF3A3.
SUBCELULAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN. SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequence of human chromosome 22."; re 402:489-495(1999).
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                                          67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15843; 1NDD.
HGNC:10765; SF3A1.
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707
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118
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369
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                                               Conservative
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7; AAC23435.1;
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                                                                                                                                                                                                                                                                                                                                                                     UBIQUITIN_2; 1.
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D., Bemis G., Bentley D., Bradshaw H., Bou
                                                                                                                                  98886
                                                               7.2%;
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                                                                                                                                  Œ.
                                             34;
                                          Pred. No. 5.8
4; Mismatches
                                                                                                                                                                        POLY-PRO.
POLY-GLU.
POLY-GLU.
POLY-PRO.
POLY-PRO.
                                                                                                                                                                                                                                                                                mRNA splicing; Nuclear SURP MOTIF 1.
SURP MOTIF 2.
UBIQUITIN-LIKE.
                                                                                     Score
                                                                                                                              POLY-PRO.
7259F1EC4577305C CRC64;
                                                                 NO 9
                                                          DB 3.8;
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                                             79;
                                                                                   Length 793;
                                             Indels
                                                                                                                                                                                                                                                                                                                                               protein; Repeat.
                                             120;
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TNR3_MOUSE
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                          EMBL; U29173; EMBL; L38423; EMBL; U30798; HSSP; O14763;
                                                                                                                                                                                                                                                         sequence trap and chromosomal mapping. ;
Genomics 30:312-319(1995).

-i- PUNCTION: Receptor for the heterotrimeric lymphotoxin containing
LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3

LTA and LTB, and role in the development of lymphoid organs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member
                                                                                                                      use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                             Honjo T.;
"The murine lymphotoxin-beta receptor cDNA: isolation sequence trap and chromosomal mapping.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CVB; TISSUE-Lung;
MEDLINE-96072804; PubMed-7594541;
Force W.R., Walter B.N., Hession
                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There
                                                                                                                                                                                                    (By similarity).
-!- SUBUNIT: Self-associates (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                          entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                Nakamura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mouse lymphotoxin-beta receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Browning J.L., Ware C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P50284;
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96163885; PubMed=8586432;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Lymphotoxin-beta receptor).
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                                     AAB00846.1;
AAA81334.1;
                                                                 AAA68964.1; -.
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Rodentia;
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STG OR CDC25 OR CG1395.

Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;

Eukaryota; Metazoa; Endopterygota; Diptera; Bracl

Insecta; Pterygota; Neoptera; Endopterygota; Drosophila.
[2]
SEQUENCE FROM N.A.
MEDLINE-91006056; PubMed-2120044;
Jimenez J., Alphey L., Nurse P., G
                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-89195217; PubMed=2702688;
Edgar B.A., O'Farrell P.H.;
"Genetic control of cell division
Cell 57:177-187(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPIP_DROME STANDARD; PRT; 479 AA. P20483; O9VAL9; O1-FEB-1991 (Rel. 17, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) M-phase inducer phosphatase (EC 3.1.3.48) (St)
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SMART; SM00208; TN
PROSITE; PS00652;
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PROSITE; PS50050; TNFR_NGFR_2;
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BY SIMILARITY
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Pred. No. 3
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RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams N.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F., RA Adams N.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Ra George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Ra George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Ra George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Ra George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Ra George R.A., Lewis S.E., Ra Haller R.G., Helt G., Nelson C.R., Miklos G.L.G., Ra Haller R.M., Basal A., Baxendale J., Bayaktaroglu L., Beasley E.M., Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burlis R.C., Barder G., Gargin S.G., Center A., Chandra I., Ra Gerson K.D., Down L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Ra Gerson K.D., Down E. G., Dunn P., Burlis R.C., Ferrisa C., Ferrisa S., Pleisohmann W., Fosler G., Gabbrielian A.E., Gargin S.S., Gelbart M.M., Glasser K., Rosler G., Gabrielian A.E., Gargin S.S., Gelbart M.M., Glasser K., Ra Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Ra Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Ra Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Ra Harris M.L., Kallah F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lai J., Lai J., Lai J., J., Lai J., J., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ra Mount S.M., Bunn M., J., Moshrefi A., Ra Mount S.M., Bunn M., Wallen H., Wang X., Ra Mang Z., Masson D.C., Scheeler F., Sh
                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; M24909; AAA28916.1; -EMBL; X57495; CAAA0732.1; -EMBL; AE003768; AAF56885.1;
PIR; A32290; A32290;
PIR; S12008; S12008.

P30304;

FlyBase; FBgn0003525; stg.
InterPro; IPR000751; MPI_Phosphatase.
InterPro; IPR000763; Rhodanese-like.
Pfam; PF00581; Rhodanese; 1.
PRINTS; PR00716; MPIPHPHTASE.

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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                          DDR1_RAT STANDARD; PRT; 910 AA.

G03474;
01-NOV-1997 (Rel. 35, Created)
11-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Epithelial discoddin domain receptor 1 precursor (EC 2.7.1.112)
(Tyrosine-protein kinase CAK) (Cell adhesion kinase) (Tyrosine kinase
DDR) (Discoddin receptor tyrosine kinase) (Protein-tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
ACT_SITE
CONFLICT
SEQUENCE
                                                                                                                                                                                                      STRAIN-Sprague-Dawley; TISSUE-Brain;
MEDLINE-94173920; PubMed-8127887;
Sanchez M.P., Tapley P., Saini S.S., He B., Pulido D., Barbacid
"Multiple tyrosine protein kinases in rat hippocampal neurons:
isolation of ptk-3, a receptor expressed in proliferative zones
the developing brain.";
                     between
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00450
Cell division;
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European
                                                                                                TYPOSINE Phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: VARIOUS EMBRYONIC AND ADULT
PROLIFERATIVE ZONES OF THE DEVELOPING BRAIN; HII
SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS
                                                                                                                                                            CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP
                                                                    SIMILARITY:
SIMILARITY:
                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                          OR EDDR1 OR PTK3
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56; Conser
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        Bioinformatics
                                                        SUBFAMILY.
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28 228
3 AA; 54094
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22.9%;
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BY SIMILARITY.
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68483F3A285962CC (
        of Bioinf
Institute.
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4; Mismatches
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Pred. No. 4.4;
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Sciurognathi; Muridae; Murinae; Rat
                                                              TYR FAMILY OF PROTEIN
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       restrictions
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    outstation -
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R1_MOUSE

DDR1_MOUSE

C 003146;

T 01-OCT-1994 (Rel. 30, Greated)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

Tothhelial discoldin domain receptor 1 precursor (EC
                                                    BERRAL
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DDR1_MOUSE
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pfam; PF00754; F5_F8_type_C; 1
ProDom; PD000001; Euk_pkinase;
SMART; SM00231; FA58C; 1.
SMART; SM00231; FYFKC; 1.
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PROSITE; PS01286; FA58C_2; 1.
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IPR000421; FA58_C.
IPR002011; RTKinaseII.
IPR001245; Tyr_pkinase.
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; Glycoprotein; Sid
ptor; ATP-binding.
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SMART; SM0023; FA58C; 1.
SMART; SM00219; TyrKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; FAL
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
PROSITE: PS01285; FA58C_1; 1.
PROSITE: PS01286; FA58C_2; 1.
                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCLITULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK I (SHOWN HERE) AND CAK ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE ABSENCE OF A 37 RESIDUES SEGMENT:
-!- TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK I, IS EXPRESSED EVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXPRESSED IN VAR EPITHELIAL CELLS.
-!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L57509; AAB05209.1;
EMBL; X57240; CAA40516.1;
PIR; S30502; S30502.
HSSP; P00523; 2PTK.
                              SIGNAL
                                                                                                                                                                                       ProDom;
                                                                                                                                                                                                                                                                                       MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                      between
                                           Alternative
                                                      Phosphorylation;
                                                                 Transferase; Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coexpressed in breast tumor cell lines Oncogene 12:1469-1477(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perez J.L., Jing S.Q., Wong T.W.;
"Identification of two isoforms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96204002;
Perez J.L., Jing :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDR1
                                                                                                                                                                                                                          nterPro; IPR000719; Euk_pkinase
interPro; IPR000421; FA58_C.
interPro; IPR002011; RTKinaseII.
interPro; IPR001245; Tyr_pkinase
                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6; TISSUE-Embryonic WEDLINE-93096484; PubMed-1281307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 766-822 FROM N.A.
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SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
                                                                                                                                                                                                                                                                                   MGI:99216; Ddr1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                  PF00069; pkinase; 1.

PF00754; F5_F8_type_C; 1.

m; PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR EDDR1
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                                                      Transmembrane;
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POTENTIAL.

EPITHELIAL DISCOIDIN DOMAIN RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                     Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              brain;
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tor; ATP-binding;
                                                                                                                                               FALSE_NEG
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Best Local S
Matches 38
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Q28181; Q28082; Q03861;

Q1-NOV-1997 (Rel. 35, Created)

Q1-NOV-1997 (Rel. 35, Last sequence update)

Q1-NOV-1997 (Rel. 40, Last annotation update)

Q20116-OCT-2001 (Rel. 40, Last annotation update)

Q2012-Signal (Rel. 40, Last annotation update)

Q2013-Signal (Rel. 40, Last annotation update)

Q2013-Signal (Rel. 35, Last sequence update)

Q2013-Signal (Rel. 35, Last sequ
MEDLINE=96198098; PubMed=8626431;
Biel M., Zong X., Ludwig A., Sautter A., I
"Molecular cloning and expression of the :
cyclic nucleotide-gated cation channel.";
J. Biol. Chem. 271:6349-6355(1996).
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SEQUENCE
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MEDLINE-96009859; PubMed-7546742;
Koerschen H.G., 11ling M., Seifert R., Sesti
Gotzes S., Colville C., Mueller F., Dose A.,
                                                                                                             TISSUE-Testis;
MEDLINE-96198098;
                                                                                                                                                                                                                  "A 240 kDa protein represents nucleotide-gated channel from Neuron 15:627-636(1995).
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NCBI_TaxID=9913;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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38; Conservative
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2; Mismatches
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photoreceptor.";
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SIMILARITY).
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                                                        Hofmann F. modulatory
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de M., Molday L.,
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Matches 35
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EMBL; X94707; CAA64367.1; --
EMBL; M61185; AAA30536.1; --
InterPro; IPR000638; M+channel_nlg.
InterPro; IPR000595; cNMP_binding.
Pfam; PF00027; cNMP_binding; 1.
Pfam; PF00520; ion_trans; 1.
SMART; SM00100; cNMP; 1.
                                                                           CONFLICT
CONFLICT
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SEQUENCE
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CARBOHYD
VARSPLIC
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PROSITE; PS00889; CNMP_BINDING_2; 1.
PROSITE; PS50042; CNMP_BINDING_3; 1.
Ionic channel; Ion transport; CAMP-b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement into removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
115 PPPSCLRFVQTNISRLL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
SEQUENCE OF 1-590 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: FORMS FUNCTIONAL HETEROOLIGOMERIC CHANNELS WITH CNG3.
SUBCELLULAR LOCATION: Integral membrane protesin.
ALTERNATIVE PRODUCTS: 3 ISOFORMS; CNG4C (SHOWN HERE), CNG4D
AND CNG4E; ARE PRODUCED BY ALTERNATIVE SPLICING. CNG4D IS BY FAR
THE MOST FREQUENT FORM (CNG4D: CNG4C: CNG4E = 20:2:1) IN TESTIS.
TISSUE SPECIFICITY: RETINA, TESTIS, KIDNEY, HEART, AND BRAIN.
SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATTON CHANNEL
FAMILY.
                              l Similarity
35; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                family; Alternative
                                                                                                                                                                                                                                                          989
1073
1094
1081
1141
                                                                                                                                                 515
522
341
454
482
572
                              Conservative
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XX-1991) to the
                                                                           AA;
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1093
1394
1219
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800
819
844
                                        7.0%;
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                                                                           155064
                          13;
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                                                                          W D R S R
                                                                                    R -> Q (IN REF. 2 AND
A -> T (IN REF. 3).
VPATEHPELQVEDADADS -
R (IN REF. 3).
S -> A (IN REF. 2).
R -> A (IN REF. 2).
D -> E (IN REF. 2).
A -> AA (IN REF. 2).
                                      Score 86.5; I
                                                                                                                                                                                                                                                                                                                    H4 (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                MISSING
K -> E (
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GLUTAMIC ACID-RICH PROTEIN.
CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4.
                           Pred. No. 18;
; Mismatches
                                                                                                                                                                                   REEEEDEEEEQD
                                                                                                                                                                                                                                              CAMP (POTENTIAL).
CAMP (POTENTIAL).
                                                                                                                                                                                                                                                                                   CYTOPLASMIC
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
H2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
H1 (POTENTIAL).
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                                                                          EE6DA559BE3744A7
                                                                                                                                                                                               E (IN REF.
                                                                                                                                                                                                                                                                    (BY SIMILARITY).
                                                                                                                                                                                                         (GLCNAC. . .) (POTENTIAL).
(IN ISOFORM CNG4E).
(IN ISOFORM CNG4D).
                                                                                                                                                                                                                                                                                (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                   DB
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                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                           53,
                                                                                                                                                                       AND
                                                  Length 1394;
                                                                                                                                                -> GSFQMSPFEALQECEALK
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ID ATF5_H
AC Q9Y2D1
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SSGP_VOLCA
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Best Local S
Matches 21
ATF5_HUMAN
Q9Y2D1; Q9UNQ3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the cellular compartment.";

J. Cell Biol. 109:3493-3501(1989).

J. Cell Biol. 109:3493-3501(1989).

FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C3Z STRUCTURE), THE COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.

-!- PIM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                                                                                      Glycoprotein; Sulfation; Hydroxylation DOMAIN 228 340 PRO-RICH. DOMAIN 260 295 POLY-PRO. SEQUENCE 485 AA; 50436 MW; A522164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE STRAIN-f. Nagariensis / HK10; MEDLINE-90094551; PubMed-2689458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vi-Aug-1991 (Rel. 19, Last sequence upol-1007-1996 (Rel. 34, Last annotation Sulfated Surface glycoprotein 185 (SSO Voluce Casteria)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSGP_VOLCA ST/
P21997;
01-AUG-1991 (Rel.
                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch)
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between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ertl H., Mengele R., Wenzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carter1: molecular structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Volvox carteri.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                   PIR; A33647; A33647.
                                                                                                                                                                                                                                                                                                                                                    EMBL; X51616; CAA35953.1; -.
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                                                                                         309 PVPPPPSPPSVL
                                                                                                                                                                               160 PDSSTLPPPWSPRPLEATAPTAPOPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGE 219
                                                                                                                     220 QVPPVPSPQDLL 231
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               STANDARD;
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19,
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29.2%;
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                                                                                                                                                                                                             Score 86; DB Pred. No. 5.9; 3; Mismatches
               PRT;
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ation update)
5 (SSG 185).
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              282 AA
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                                                                                                                                                                                                                                           Length 485;
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CONFLICT
SEQUENCE
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Human Cdc34 and Rad6B ubiquitin-conjugating enzymes target repr
"Human Cdc34 and Rad6B ubiquitin-conjugating enzymes target repr
of cyclic AMP-induced transcription for proteolysis.";
Mol. Cell. Biol. 19:5001-5013(1999).
-1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE)
(CONSENSUSS: 5'CTGACGT(A/C)(A/G)-3'), A SEQUENCE PRESENT IN M
VIRAL AND CELLULAR PROMOTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cyclic-AMP-dependent transcription factor ATF-5
transcription factor 5) (Transcription factor A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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TRANSFAC; T04877; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20558615; PubMed-11087824; White J.H., McIllhinney R.A.J., Wise A., Emson P.C., Billinton A., Warshall F.H.; "The GABAB receptor interacts directly wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                         DNA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:790; ATF5
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  179
                                                                                   144 WIT-RONESRCLELQCQPDSSTLPPPWSPRP--LEATA-----
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                                       WMTERVDFTALLPLEPPLPPGTLPQP-SPTPPDLEAMASLLKKELEQMEDFFLDAPPLPP.124
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AB021663; BAA78477.
                                                                                                                                                                                                                                                                                                                                                                                                                             SM00338; BRLZ;
                                                                                                                                    . Similarity
38; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREB2 and ATFx.";
atl. Acad. Sci. U.S.A. 97:13967-13972(2000)
                                                                                                                                                                                                                                                                                                                                                                                                      PS00036; BZIP_BASIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DEC-1998) to the
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210
236
161
282
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Primates;
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DNA-binding;
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POLY-PRO.
BASIC MOTIF.
LEUCINE-ZIPPER (PROE
LLA -> RHE (IN REF.
LLA -> DDBZF907CA0215A0 C
                                                                                                                             Score 85; DB Pred. No. 3.9; 7; Mismatches
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                                                                                                                               38;
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                                                                                                                                                                         Length 282
                                                                                                                                                                                                                     CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WITH GABAB
                                                                                                                                                                                                                                                                                                                                                                             protein;
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                                                                                                                               44;
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                                                                                                                             Gaps
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                                                                                                                                                                   STRUCTURE 6:63-73(1998).

STRUCTURE 6:63-73(1998).

STRUCTURE 6:63-73(1998).

STRUCTURE 6:63-73(1998).

STRUCTURE FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS GAMMA. MEDIATES THE SELECTIVE UPTAKE OF IGE FROM MILK AND HELPS NEWBORN ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGG IN THE MILK IS BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE RESULTANT FCRN-IGG COMPLEXES ARE TRANSCYTOSED ACROSS THE INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCRN INTO BLOOD C TISSUE FLUIDS (BY SIMILARITY).

-I- SUBBNIT: FCRN COMPLEX CONSIST OF TWO SUBUNITS: P51, AND P14 WHICH IS EQUIVALENT TO BETA-2-MICROGLOBULIN. IT FORMS AN MCH CLASS I-
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95059482; PubMeBurmeister W.P., Huber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simister N.E., Mostov K.E., "Cloning and expression of the neonatal rat intestinal Fc major histocompattbility complex class I antigen homolog." Cold Spring Harb. Symp. Quant. Biol. 54:571-580(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Epithelium;
MEDLINE-90315866; PubMed-2534798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FCGN_RAT P13599;
                                                                                                                                                                                                                                                                                                                                      Vaughn D.E., Bjor)
"Structural basis
                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
MEDLINE=98154319; PubMed=9493268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "An Fc receptor structurally related Nature 337:184-187(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simister N.E., Mostov K.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor) (IGO FCGRT OR FCRN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGG receptor FCRN receptor) (IGG FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990
01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Crystal structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89097257; PubMed-2911353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                             Nature 372:379-383(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 VPPVPSP
                                                                                                                LIKE HETERODIMER.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: INTESTINAL EPITHELIUM.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
                                                                              SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
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basis of p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13, Last sequence update)
41, Last annotation update)
large subunit PSI precursor (FCRN)
fragment receptor transporter, alph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=7969498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                         of the
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                      pH-dependent antibody binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                       complex of rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Sciurognathi; Muridae;
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                                                                                                                                                                                            P14 WHICH
                                                                                 collaboration
                                                                                                                                                                                                                        BLOOD OR
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Query Match
Best Local
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16-OCT-2001 (Rel. 40, Last sequence
16-OCT-2001 (Rel. 40, Last annotati
16-OCT-2001 (Rel. 40, Last annotati
Alpha-fetoprotein enhancer binding
(AT-binding transcription factor 1)
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InterPro; IPR003597; Ig_cl.
InterPro; IPR001039; MHC_I.
Pfam; PF00047; Ig; 1.
Pfam; PF000129; MHC_I; 1.
ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGcl; 1.
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EMBL; M35495; AAA41611
PIR; S02117; S02117.
PIR; A37374; A37374.
PDB; 1FRT; 14-FEB-95.
PDB; 3FRU; 10-JUN-98.
    SEQUENCE FROM N.A.
STRAIN-BALB/MK X ICR; TISSUE-Brain;
MEDLINE-96194902; PubMed-8654949;
Ido A., Miura Y., Watanabe M., Sakai
Hashimoto T., Morinaga T., Nishi S.,
                                                                                                                                                                                                                                                                                                                                                                MOUSE
ABF1_)
Hashimoto
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 LLLLA---AAWCLHWQRTRRRTPR------PGEQVPPVPSPQ 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 RKESEFLLTSCP-----ERLIGHLERGRONLEWKEPPSMRLKARPGNSGSSVL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TCAAFSFYPPELKFRFLRNGLA------SGSGNCSTGPN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTEIHFVTKCA---FQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RELSDYLLQDYPYTVASNLQDEELCGGLWRLVLAQRWME----RLKTVAGSKMQGLLERV 101
                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 22.:
51; Conservative
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                                                                                                                                                                                             (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAA32503.1;
AAA41611.1;
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                                                                                                                                                                                                              .. 40, Created)
1. 40, Last sequence update)
1. 40, Last annotation update)
in enhancer binding protein (Af
                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 85;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
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N-LINKED (GLCNAC. . .)
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                                                                                                                                             Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                            3726 AA
        M., Inoue
Tamaoki T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 366;
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                           Miki T.,
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) (POTENTIAL).
                                                                                                                                                                   Euteleostomi;
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                                                                                                                                                  Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT P51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
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                                                                                                                                                                                                                                                     factor)
                                                                                                                                                Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
    TRANSFAC: 103881;
MGI: 9948; Atbfl.
MGI: 9948; Atbfl.
InterPro; IPR001356; Homeobox.
InterPro; IPR001822; Znf_C2H2.
InterPro; IPR003604; Znf_U1.
Pfam; PF00046; homeobox; 4.
Pfam; PF00096; zf-C2H2; 20.
PF0D0m; PD000010; Homeobox; 4.
SMART; SM00355; ZnF_C2H2; 22.
SMART; SM00351; ZnF_U1; 7.
                     ZN_FING
ZN_FIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding;
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00027; HOMEOBOX_1; 2.
PROSITE; PS00071; HOMEOBOX_2; 4.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 15.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D26046; BAA05046.1; -.
HSSP; P20263; 10CP.
TRANSFAC; T03881; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: Transcriptional activator that binds to the sequence of the enhancer element of the AFP gene. -!- SUBCELLULAR LOCATION: Nuclear. -!- SIMILARITY: CONTAINS 4 HOMEOBOX DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning of the cDNA encoding the mouse ATBF1 transcription factor."; Gene 168:227-231(1996).
-!- FUNCTION: Transcriptional activator that binds to the AT-rich cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription
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Nuclear protein;
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C2H2-TYPE (DEGENERATE).
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RESULT

SQ FT	DOMAIN 3620 3623 POLY-PRO. DOMAIN 3659 3662 POLY-SER. SEQUENCE 3726 AA; 406567 MW; 915ACBE588A72C98 CRC64;
¥ # 5	Query Match 6.8%; Score 84.5; DB 1; Length 3726; Best Local Similarity 21.6%; Pred. No. 80; Matches 53; Conservative 29; Mismatches 70; Indels 93; Gaps 12;
Qy	29 DCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 86
Ф	3033 ECTLCGIKYSARLSVRDHIFSQQHISKVKDTIGSQLDKEKEYFDPATVRQLMAQQELDRI 3092
Qy	87 KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTN 126
뫄	3093 KKANEVLGLAAQQQGMFDNAPLQALNLPTTYPALQGIPPVLLPGLNRPSLPGETPAN 3149
Qy	127 ISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWS 170
뫄	3150 TALTSPKPNLMGLP-STTVPSPGLPTSGLPNKPSSASLSS 3188
Qy	PLLLLLLPVGLLLLAAAWCLHWQRTF
Db	3189 PTPAQATMAMAPQPP
γo	224 VPSPQ 228
Дb	3225 IPAPQ 3229
Search	Search completed: May 27, 2003, 18:27:34

Job time : 15 secs

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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                 602.5
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_mammal:*
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Q17889
Q8VD70
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Q8VCH4
Q9LGG8
Q9GY11
Q9GY33
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Q9N753
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Q9MZU9
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O9mzu9 felis silve
O9gke0 bos taurus
O8wnw1 bos taurus
O9gkd9 bos taurus
Of1104 mus musculu
O8vch4 mus musculu
O9vch4 mus musculu
O9lg98 oryza sativ
O9lg98 leishmania
O9gy31 leishmania
O9gy33 leishmania
O9wim6 mus musculu
O9n753 leishmania
O9n753 leishmania
O9dwh8 rat cytomeg
O9c5t0 arabidopsis
O17889 caenorhabdi
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6.8	6				0	6	6.9	6.9	7.0	7.0	7.0	7.0	7.0	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.2	7.3	7.3	7.3	7.4	7.4	7.4
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homo	mus musculu	caulobacter	homo sapien	ct	mus musculu	()		mug	bos taurus	hemicentrot	leishmania	cylindroth	arabidopsi		a u	sus scrofa	homo s		oryza sativ	3	anabaena sp	caenorhabdi	gallus gal	leishmania	leishmania	homo sapien	drosophila	leishmania
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ALIGNMENTS

												
Qy 61 ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMGGLLERVNTEIHFVTKCAFQPDPSCL 120	1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPY	Query Match 72.1%; Score 895.5; DB 6; Length 294; Best Local Similarity 77.1%; Pred. No. 3.5e-80; Matches 182; Conservative 12; Mismatches 35; Indels 7; Gaps	DR EMBL; AF155148; AAF87088.1; DR InterPro: TDR004213: E1+3 147	-	 •	RP SEQUENCE FROM N.A. Philmpd-10902925.	; Fissipedia; Canidae;	Flt3 ligand.	DT 01-0C1-2000 (TrEMBErel. 15, Last sequence update) DT 01-JUN-2002 (TrEMBErel. 21, Last annotation update)	01-OCT-2000 (TrEMBLrel. 15,	ID Q9MZVO PRELIMINARY; PRT; 294 AA.	RESULT 1
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B 5

181

APQPP-LLLLLLPVGLLLLAAAWCLHW-QRTRRRTPRPGEQVPPVPS-----

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RFVQTNISHLLQDTSQQLAALKPWITRRNFSGCLELQCQPDSSTLVPPRSPGALEATALP 180

APQAPRILLLILLPVALLIMSTAWCIHWRRRRRRRSPYPGEQRTIRPSERSHIPED 236

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RESULT
Q9GKE0
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Best Local S
Matches 178
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Q9GKE0;
01-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, L
01-DEC-2001 (TrEMBLrel. 19, L
Flt3 ligand isoform-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              long cytoplasmic domain.";
DNA Seq. 11:163-166(2000).
EMBL; AF155149; AAF87089.1; -
InterPro; IPR004213; F1t3_11g.
Pfam; PF02947; f1t3_11g; T
SEQUENCE 291 AA; 32459 MW; 8
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Q9MZU9;
01-OCT-2000
01-OCT-2000
01-JUN-2002
F1t3 ligand.
SEQUENCE FROM N.A.

MEDLINE-20570936; PubMed-11120823;

MWang1 W., Brown W.C., Palmer G.H.;

"Identification of fetal liver tyrosine kinase 3 (Flt3) ligand required for receptor binding and function using naturally occu
                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Felis silvestris catus (Cat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;

NCBi_TaxID-9685;
                                                                                                                                                                           NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning of canine and feline flt3 ligand reveals high degree of similarity to the human and mouse homologue but uniquely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-20358731; PubMed-10902925;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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Last sequence update)
Last annotation update)
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Pred. No. 4.3e-80;
9; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Best Loc
Matches
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Best Local
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01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                 Submitted (NOV-2000) to the EMBL/GenBank/DDBJ EMBL; AB051841; BAB79634.1; -. InterPro; IPR0044213; F113_11g. Pfam; PF02947; f113_11g; 1. SEQUENCE 292 AA; 32388 MW; 2A797E0C1199C11
                                                                                                                                                                                                                                                                                                                                                                                                                   Flt3
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                                                                                                                                                                                                                                                                                   Hikono H., Momotani E.; "Cloning of a cDNA for bovine flt3 ligand."; Submitted (NOV-2000) to the EMBL/GenBank/DDE
                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Cetartiodactyla; Rur
Bovidae; Bovinae; Bos.
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01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                       FLT3 LIGAND.
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                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913
 181
                                             121
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                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
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                                                                                                    VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMOGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGPQSPLLLLLLLLPVALLLLATAWCLCRWRRRRRTRYPGER
                   TAPQPP----LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQ
                                                                                       VASNLQDDKLCGAFWRLVLAQRWMGRLKTVAGSEMEKLLEDVNTEIHFVTSCAFQPLPSC
                                                                                                                                                                                                                                                                                                                                                                                                                 ligand.
PGPQSPLLLLLLLLLPVALLLLATAWCLCRWRRRRRTRYPGER
                                           LRFVQANISHLLQDTHQQLEALKPWITHRNFSRCLELQCQPDSPTLLPPRSPGALGATSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAPQPP----LLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LREVOTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAP 179
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                                                                                                                                                                                       170;
                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                67.2%;
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76.38;
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                                                                                                                                                                                     12;
                                                                                                                                                                                    Score 835; DB
Pred. No. 3.2e
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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Pred. No. 1e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D68B9ED79221202D CRC64;
                                                                                                                                                                                                                                    2A797E0C1199C1D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                  ta; Vertebrata; Euteleostomi;
Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292
                                                                                                                                                                                                DB 6;
.2e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
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                                                                                                                                                                                                           Length 292;
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224
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                    McClanahan T., Culpepper J., Campbel Mattson J., Tsai S., Luh J., Guimare Birnbaum D., Hannum C.; genomic or forms and processing.", Submitted (DEC-1995) to the EMBL/Ger EMBL; U44024; AAA93305.1; EMBL; U44024; AAA93305.1; InterPro; IPR001230; Prenyl_site. Pfam; PF02947; fil3_lig. InterPro; IPR001230; Prenyl_site.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                             FLT3L.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001
01-MAR-2001
01-DEC-2001
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01-NOV-1996 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Fit3 ligand, T169 form.
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MEDLINE=20570936; PubMed=11120823;

Mwangi W., Brown W.C., Palmer G.H.;

"Identification of fetal liver tyrosine kinase

"Identification of fetal liver tyrosine winase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute:
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   required for receptor ligand isoforms.";
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                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
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AR-2001 (TrEMBLrel. 16,
EC-2001 (TrEMBLrel. 19,
ligand isoform-2.
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ilarity 69.6%;
Conservative 1
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PRENYLATION; UNKNOWN_1
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Last annotation updat
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                                                                                                                                                                                                                                                                                     Campbell
Guimares
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Pred. No. 1.8e
12; Mismatches
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Last sequence update)
Last annotation update)
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Sciurognathi; Muridae;
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1.8e-65;
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                                                                                                                                                                                                                                                                                     Wagner J.
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                                                                                                                                                                                                                                                                                  ., Franz-Bacon
M.-G., Rosnet
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Murinae;
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     O9LGG8 PRELIMINARY; PRT; 579 AA.
C 09LGG8;
T 01-OCT-2000 (TrEMBLrel. 15, Created)
T 01-UN-2000 (TrEMBLrel. 15, Last sequence update)
T 01-UN-2002 (TrEMBLrel. 21, Last annotation update)
T 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
P PUTATIVE extensin-like protein.
P PO406H10.6 OR OJI174_D05.5.
N P0406H10.6 OR OJI174_D05.5.
S Oryza sativa (Rice).
C Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
C Spermatophyta; Magnoliophyta; Liliopsida; Poales; Po
C Ehrhartoideae; Oryzaa.
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8VCH4;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to FMS-11ke tyrosine kinase 3 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2001) to the EMBL/GenBank/DDBJ EMBL; BC019801; AAH19801.1; ... InterPro; IPR004213; Flt3_119. Pfam; PF02947; flt3_119; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg
Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8VCH4
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                                                                                                                                                                                                     LREVQTNISRLLQETSEQLVALKPWITR--QNFSRCLELQCQPDSSTLPPPWSPR 172
                                                                                                                                                                                                                                                                                                   MTVLAPAWSP-TTYLLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPYT
                                                                                                                                                                                                                                                   VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
                                                                                                                                                                                        LRFVQTNISHLLKDTCTQLLALKPCIGKACQNFSRCLE----
                                                                                                                                                                                                                                         VAVNLQDEKHCKALWSLFLAQRWIEQLKTVAGSKMQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                       MTVLAPAWSPNSSLLLLLLLLSPCLRGTPDCYFSHSPISSNFKVKFRELTDHLLKDYPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LREVQTNISHLLKDTCTQLLALKPCIGKACQNESRCLEVQCQPDRVSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAVNLQDEKHCKALMSLFLAQRWIEQLKTVAGSKNQTLLEDVNTEIHFVTSCTFQPLPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSC
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                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      169 AA; 18986 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.5%; Sco
72.6%; Pre
**ive 15;
                                                                                                                                                                                                                                                                                                                                                    46.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19465 MW;
                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                     Score 578; DB 11;
Pred. No. 3.7e-49;
4; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 602.5;
Pred. No. 1.5e
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                      5B4CA47D9724EFF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04F0A010171E3384 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169
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                     Embryophyta; Tracheophyta;
a; Poales; Poaceae;
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                                                                               update)
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Best Local S
Matches 54
         SEQUENCE FROM N.A.

STRAIN-FRIEDLIN;

STRAIN-FRIEDLIN;

STRAIN-FRIEDLIN,

STRAIN-FRIEDLIN,

MUTPhy L. Quail M., Harris D., Rajandream M., Iv

Oliver K.;

Oliver K.;

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ dail

EMBL; AL390114; CAC02038.2; -

InterPro; IPR000561; EGF-11ke.

InterPro; IPR001561; LRR:

InterPro; IPR001561; LRR:

InterPro; IPR0023955; P_rich_extensn.

PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00181; ESF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9GY11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Oryza sativa nipponbare(GA3) genomic clone:0/1174_D05.";
                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9GY11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01582; KV33CHANNEL.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00370; LRR; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic clone:P0406H10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
SEQUENCE 579 AA; 62607 MW; 04457E18
                                                                                                                                                                                                                                                                                                                eishmania major.
Sukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                    Probable surface antigen
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InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           CBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAPOPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NI--SRLLQETSEQLVALKPWITRQNESR----CLELQCQPDSSTLPPPWSPRPLEATAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQ-----PPPSCLRFV-----QT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                Kinetoplastida;
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18,
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                             Trypanosomatidae;
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                                                                                                                                                                                                 Barrell
                                                                                                                                                                                                                                                                                                                Leishmania.
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Best Local S
Matches 63
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Matches
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01-MAR-2001
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases EMBL; AL390114; CAC02017.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Murphy L., Quail M., Oliver K.;
                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000561;
InterPro; IPR001611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-FRIEDLIN;
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                                                    289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 LPPEWSSMPNLQTLQVRRLKLSGT-----LPADWS-SLKSLSNVVLEDMPIT----
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                                                                                                                                                                                                                                                              Local Similarity les 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
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                                                                                                 ALRELTLDGTNLSGTLPPQWSAMASVISLNLEGTEVSGTLPPEWISMSRL-QTLNLRRTK
                                                                                                                              CLREVQ---TNISRLLQ-----
                                                                                                                                                        -----GL----LPPEW
                                                                                                                                                                                                         LPPEWSSMPNLNAVELKRLKLSGT------LPADWS-SLKSLSNVVLEDMPIT----
                                                                                                                                                                                                                                  LAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASN 63
                                                 VSGTLPPEWSSMGSLANLQLSLTQVSGTLPPQWSSMKKLTQLLLTDTLLSGTLPAEW 345
                                                                           DSSTLPPPWSPR----PLEATAPTAPQPP----
                                                                                                                                                                                LQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPP-----S 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSGTLPPEWSSMGSLANLQLSLTQVSGTLPPQWSSMRKLTQLLLTDTLLSGTLPAEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GL----LPPEW-----
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                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                           PRICHEXTENSN
                                                                                                                                                                                                                                                                                                                 68470 MW;
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                                                                                                                                                                                                                                                                                                                                                                  P_rich_extensn.
                                                                                                                                                                                                                                                                        8.3%; Score 102.5; D
26.6%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                              EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.4%; Score 104.5; DB 26.6%; Pred. No. 0.093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kinetoplastida; Trypanosomatidae; Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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                                                                                                                                                                                                                                                                                                              8EB78AC101E01286 CRC64;
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                                                                                                                                                      -GSLERIQQLVLRKLKVTGPLPPQWSPMK 229
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                                                                           -LLLLLLPVGLL--LLAAAW
                                                                                                                                                                                                                                                                                      DB 5;
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Best Local S
Matches 70
Submitted (AUG-2001) to the EM
EMBL; AL390114; CAB98658.2; -.
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR_out.
Pfam: PF00560; LRR; 3.
SMART; SM00370; LRR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TremBLrel 01-OCT-2001 (TremBLrel 01-DEC-2001 (TremBLrel
                                                                                                                                                                                                                                                                Murphy L., Quail M., Oliver K.;
                                                                                                                                                                                                                                                                                                                                         STRAIN-FRIEDLIN,
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probable surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9N753;
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01-MAR-2002
01-JUN-2002
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EMBL; AF375593; AAL35321.1; ...
MGD; MGI:2153816; Strc.
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21547528; PubMed-11687802;
Verpy E., Masmoudi S., Zwaenepoel I., Leibovici M., H.
Del Castillo I., Nouaille S., Blanchard S., Laine S.,
Moreno F., Mueller R.F., Petit C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB/C;
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                                                                                                                                                                                                                                                                                          Harris D.,
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23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinetoplastida; Trypanosomatidae;
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18,
19,
n p2
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Last annotation update)
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Pred. No. 0.74;
5; Mismatches
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                 Rajandream
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                                                                                                                                                                                                                                                                                 Ivens A.,
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                                                                                                                                                                                                                                                                                     Barrell
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Best Local Similarity
Matches 56; Conserv
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STRAIN-MAASTRICHT;
MEDLINE-20473137; PubMed-11018281;
MEDLINE-20473137; PubMed-11018281;
Gruijthuijsen Y.K., Beuken E., Bruggeman C.A.,
Gruijthuijsen Y.K., Beuken E., Bruggeman C.A.,
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01-MAR-2001
01-DEC-2001
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Virus Res. 69:119-130(2000).
EMBL; AF232689; AAF99111.1; -.
SEQUENCE 1240 AA; 125612 MW;
                                                                                                                                                                                                                                                                                                               160
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MEDLINE-20366325;
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Betaherpesvirinae; Muromegalovirus
NCBI_TaxID=79700;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEDLINE-20366325; PubMed-10906222;
Vink C., Beuken E., Bruggeman C.A.;
Complete DNA sequence of the rat cytomegalovirus
, Virol. 74:7656-7665(2000).
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                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                            PDSSTAVTGEATTERSTPATEPRPYRPLPPGVDSALPLAPQPITLLSLLLVPA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAWSPTTYLLLLLLSSGLSGT---------QDCSFQHSPISSDFAVKIRELS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSRLPQPALRHRLN-----PQPPLRHRLNPRPLLP----
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16,
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RNA stage; H
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Q9C5T0; Q9C5T0; 01-JUN-2001 01-JUN-2001

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Created) Last sequ

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Best Local S
Matches 34
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Pfam; PP01657; DUP26; 2.
Pfam; PP00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Transferase.
                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-MAR-2002 (TrEMBLrel. 2
F54F12.1 protein.
                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID-6239;
"Gename sequence of the nematode investigating biology."; Science 282:2012-2018(1998). EMBL; Z8f548; CABO4464.1; -.
                                                    none;
                                                              SEQUENCE FROM N.A. MEDLINE-99069613; PubMed-9851916;
                                                                                                    Submitted (NOV-1996)
                                                                                                                 Barlow
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                   017889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of genes encoding receptor-like protein kinases as possible targets of pathogen- and salicylic acid-induced WRKY DNA-binding proteins in Arabidopsis."; Plant J. 24:837-847(2000).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=20575726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Receptor-like protein kinase 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro; IPR000719;
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1 Similarity 25.8%;
34; Conservative 1
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                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Ser_thr_pkinase.
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Last sequence update)
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Pred. No. 1.1;
16; Mismatches
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                                     C.elegans: A
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Search completed: May Job time : 38 secs
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InterPro; IPR000242; Tyr_pp.
Pfam; PF00102; Y_phosphatase; 1.
SMART; SM00194; PTPC; 1.
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                                             GAVGGLLVVAIIGVILFFVFFQKKKKKEDKPDD--PPAPLP
                                                                   LPVGLLLLAA----AWCLHWQRTRRRTPRPGEQVPPVPSP
                                                                                                                                                              MERLKTVAGSKMQGL---LERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLV 139
                                                                                                              ALKPWITRQNFSRCLELQCQPDSSTL---PPPWSPRPLEATAPTAP---
                                                                                                                                     MDAVKAVDGTKYSSVIDALEKLSTMDLDFQKYKFKEAPATLKAMDL---
                                                                                        ALRPQPTTSDPTAAAPVPIPNNKGSLNGNPSPSSPPLLPPVASSTPAATPEESNMLLYII
                                                                                                                                                                                     Similarity
38; Conserv
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            27,
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TYR_PHOSPHATASE_2; 1
TYR_PHOSPHATASE_PTP;
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2.6;
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Result
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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1242
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|: /SIDS2/gcgdata/
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6	Score	Match Length DB	ength I		Ī		Description
-	1242	100.0	235	16	AAR67541		Human flt-3 ligand
N	1242	100.0	235	20	AAW67769		Human flt3:ligand
w	1242	100.0	235	21	AAY69719		Full length wild t
4	1242	100.0	235	22	AAB20192		Human Flt-3 ligand
ۍ.	1242	100.0	235	23	ABB08129		Human Fital polyne
σ	1236	99.5	235	16	AAR66175	÷	Human S86/S109 F1+
7	1236	99.5	235	22	AAB20194	÷	Human Flt-3 ligand
œ	1124	90.5	212	2	AAY69721		Human flt 3 mutein
9	1114	89.7	209	19	AAW69007		Human flt-3 recent
10	1114	89.7	209	21	AAY69720		Mature wild type h

	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	Ľ
	735	735	735	735	735	36	736.5	36	37	1.3	739	739	740.5	745	745	764	768	768.5	768.5	33	9	96	9	_	894.5	in	970	1100	. 1107	1108	1108	1110	1110	1110	1110
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														19	19	22	16	22	20	16	21	21	21	22	21	21	22	21	21	21	21	21	21	21	21
	AAW83294	AAW69052	AAW77928	AAW69035	AAW77911	AAW78008	AAW83286	AAW83291	AAW78005	AAW83289	AAW69050	AAW77926	AAW78124	AAW69054	AAW77930	AAB20189	AAR66177	AAB20186	AAW67768	AAR67540	AAY58211	AAY58207	AAY58206	AAB20193	AAY58210	AAY58204	AAB20195	AAY69725	AAY69728	AAY69724	6972	6972	6972	Y697	AAY69723
•	Human flt3 l	Human flt-3	Flt3 ligand	Human flt-	Human flt3	Trimer	Human flt3	Human flt3	F1t3L 1-13	Human flt3	Human fit-:	Flt3 ligan	Chimeric rec	an fit-3	_	e F1t-3	e MoT110	F1t-3	e flt3-1:	flt-3 1	matu	F1t-1	e mat	F1t-3	Flt.	ne Flt-3	F1t-3	flt-3	f1t-3	flt-3	flt-3	f1t-3	f1t-3	n flt-3	Human flt-3 mutein

ALIGNMENTS

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19-MAY-1994;	07-DEC-1994.	EP627487-A.		DOMA in	Domain	•		Domain	•		Peptide	Key	. •	Homo sapiens.	Flt-3 ligand;		Human flt-3 li	05-AUG-1995 (AAR67541;	RESULT 1 AAR67541 ID AAR67541 stand XX	
94EP-0303575.		•	/label= Cytoplasmic_domain	/label- Transmembrane_domain	183205	position 28"	Extracellular_domain		-	/label- Sig_peptide	126	Location/Qualifiers		•	<pre>Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.</pre>		ligand.	(first entry)			T 1 541 AAR67541 standard; Protein; 235 AA.	

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                               Antigen-specific peripheral immune tolerance; flt3-ligand; immunogenic; autoimmune disease; organ transplantation; for tissue transplantation.
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12-AUG-1993;
25-AUG-1993;
(IMMV ) IMMUNEX CORP.
                                                                23-DEC-1998
                                                                                     WO9857655-A1
                                                                                                          Homo sapiens
                                                                                                                                                                          Human flt3-ligand
                                                                                                                                                                                               25-MAR-1999
                                                                                                                                                                                                                     AAW67769
                                                                                                                                                                                                                                      AAW67769 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A human T-cell lambda-gtl0 random primed cDNA library was screened with a fragment corresponding to the extracellular domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAQ79076) to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 29-30; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated ligands for flt 3 receptors - useful for treating anaemia, AIDS and various cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ79079.
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07-MAR-1994;
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                                                                                                                                                                                                                                                                                         APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                                                                                                                                                                                                                                   RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
                                                                                                                                                                                                                                                                                                                                                                              ASNIQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
                                                                                                                                                                                                                                                                                                                                                                                             ASNLQDEELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells, and can be used e.g. in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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93US-0106463.
93US-0111758.
93US-0162407.
94US-0209502.
94US-0243545.
                     97US-0877421
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                                                                                                                                                                                            entry)
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Pred. No. 5e-109;
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RESULT 3
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Best Local S
Matches 235
                                                                                                                  Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoitet progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or therapeutic molecule, respectively. The polypeptide is capable of binding the flt3 receptor and is: a) amino acids 28 x of murine flt3 ligand (flt3-L), where x is an amino acid between 163-231; b) amino acids 28 y of human flt3-L, where y is an amino acid between 160-235; and c) a polypeptide that has at least 90% identity to the polypeptides of either (a) or (b). The method ameliorates the effects of autoimmune transplantation. Administration of flt3-L allows lower doses of antigens to be used in vivo for mucosally administered antigens. The present sequence represents human flt3-L.
                                                                                                        multiple myeloma; leukemia.
                                                                            Homo sapiens
                                                                                                                                                                                                                                                                        05-JUL-2000
                                                                                                                                                                                                                                   Full length wild type human flt-3 protein.
                                                                                                                                                                                                                                                                                                                                  AAY69719 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A method has been developed of initiating or enhancing: (1) an antic
specific immune tolerance; or (ii) immunotolerance of a therapeutic
immunogenic molecule by addition of a polypeptide, before, after or
the mucosal administration of an immunotolerising amount of the anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A method
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Pred. No. 5e-109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel soluble fit3 ligand (fit3-1) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (this sequence) or mature (AAK99720) fit3-1 cplypeptides. The fit3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoietic progenitor cells. The fit3-L protein can be used to induce cellular of the fit3-L protein can be used to induce cellular of the matopoietic carpansion (especially in vivo) or differentiation, e.g. the control of the matopoietic natural killer (NK) or dendritic cells, especially in the carpansion (especially in the carpansion (especially in the control of growth factors such as interlevkins, colony stimulating capteence of growth factors such as interlevkins, colony stimulating capteence of growth factors such as interlevkins, colony stimulating control of a patient's immune response and can be used to treat an immune color of immunosuppression). The protein capter (e.g. allergy, autoimmunity or immunosuppression). The protein color of the used to treat a pathological condition e.g. myelodysplasia, and can be used to treat a pathological condition e.g. myelodysplasia, color of the color of the capter of the color of th
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Best Local S
Matches 235
         Filt-3 ligand; Fms-like tyrosine kinase; human; vaccine; immunotherapy; therapy; tumour; cancer; melanoma; glioma; lymphoma; autoimmune disease; infection; gene therapy. Homo sapiens.
                                                                                                                                                                                                                Human Flt-3
                                                                                                                                                                                                                                                                         14-MAY-2001
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235; Conser
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                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein;
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Query Match Best Local S Matches 235

Similarity

100.0%;

Score 1242; DB 2 Pred. No. 5e-109; Mismatches

DB 22; 0;

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Sequence

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The present sequence is that of human Fms-like tyrosine kinase CC [Fit-3 ligand]. The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytckine by CC administering in vivo, into a tissue of a vertebrate, a Fit-3 CC ligand-encoding polynucleotides. The Fit-3 ligand-encoding croytokine-encoding polynucleotides. The Fit-3 ligand-encoding polynucleotides. The Fit-3 ligand-encoding polynucleotides are incorporated conjuncted may encode the present full-length human Fit-3 (19and polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185, CC (19and polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185, CC (19and polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185, CC (19and polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185, CC (19and polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185, CC (19and polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185, CC (20and polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185, CC (20and or cytokines is produced in vivo, and a prophylactical compositions comprising the polynucleotides are useful for CC (20and or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for CC (20and or lymphoma, particularly B-cell lymphoma. The tumour is melanoma, CC (20and or lymphoma, particularly B-cell lymphoma. The tament of CC (20and or humans), parasitic (e.g. malaria) and fungal infections; CC (20and or humans), parasitic (e.g. malaria) and fungal infections; CC (20and or humans), parasitic (e.g. malaria) and fungal infections; CC (20and or humans), concer; and (d) Aujeszky's disease in pigs. CC (19and or humans) are concer; and (d) Aujeszky's disease in pigs. CC (20and or humans) are disease are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic compositions comprising Fit-3 ligand encoding polynucleotide and one or more antigen, or cytokine encodipolynucleotides, useful for suppressing tumour growth and autoimmune diseases (e.g. rheumatoid arthritis)
specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 132-133; 149pp; English
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N-PSDB; AAF30310.
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The invention relates to treating an individual at risk for or suffering from infection with a pathogenic or opportunistic organism. The method convolves administering a combination of two-to-trive agents presented and involves administering a combination of two-to-trive agents comprising:

CC agent; (c) dendritic cell activation agent; (d) The delimitic cell maturation correctly an individual activation agent; (d) The delimitic cell maturation correctly an individual at risk for or suffering from infection with a cell gent correctly with a cell gent cel
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RESULT 6
AAR66175
              C A cDNA library from the human stromal cell line 29SV48, in pME18S, was screened with an 800 bp fragment derived from mouse clone T118. This fragment encompasses the coding region conserved between two mouse clones, T118 and T110. Approx. 20 positive clones were selected and partially sequenced. Two clones, S86 and S109, were found to be approx. 75% homologous to the mouse clones over the first 163 AAs. Clone S86 continued to show homology to T110 until the stop codon, although to a lesser degree, for an overall homology of 66%. Clones T118 and S109 do not show homology to each other or to the other clones after mouse residue 163 (human residue 160). An additiona mouse clone designated MB8 has a 29 AA insert at the junction between the common and divergent portions of the mouse ligand.
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07-JUL-1993;
16-JUL-1993;
13-AUG-1993;
24-AUG-1993;
19-NOV-1993;
                                                                                                                                                                                                    Claim 11; Page 76-77; 90pp; English.
                                                                                                                                                                                                                          New ligand for the Flt3 tyrosine kinase receptor - and relationucleic acid, vectors, host cells and antibodies, useful for treating abnormal cell physiology and proliferation, e.g. calalso for diagnosis and drug screening
                                                                                                                                                                                                                                                                                              WPI; 1995-006787/01.
N-PSDB; AAQ79642.
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93US-0089263.
93US-0092549.
93US-0106340.
93US-0112391.
93US-0155111.
93US-0162413.
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RESULT 7
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      The present sequence (Flt-3 ligand). The
                                                                                                            autoimmune
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                                                                                                                                             Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding
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DB; AAF30312.
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27..235
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                                                                                                                           nd one or more antigen, useful for suppressing
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is that of human Fms-like tyrosine invention is directed to enhancing
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02-JUL-1998;

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25-JUN-1999; 13-JAN-2000 WO200001823-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 compositions comprising the polynucleotides are useful for more antigen or a cytokine by the cells of the vertebrate, a fit-3 cytokine-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The fit-3 ligand-encoding polynucleotides are full-length human fit-3 cytokine-encoding polynucleotides. The fit-3 ligand-encoding polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of fit-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumour growth in a mammal. The tumour is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of:

(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and continuous diseases (e.g. rheumatoid arthritis and infections);

(b) autoimmune diseases (e.g. rheumatoid arthritis and costeoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 234
                                                                                                                                                                                                                         Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoietic progenitor cell; cellular expansion; cellular differentiation; natural killer cell;
                                                                                                                                     Homo sapiens.
Synthetic.
                                                                                                                                                                               cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma; multiple myeloma; leukemia; mutein.
                                                                                                                                                                                                                                                                                                          Human flt-3 mutein L-3H.
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                                                                                                                                                                                                                                                                                                                                                                                                       AAY69721 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234;
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Pred.
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No. 1.8e-108;
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Human; flt-3 receptor agonist; haematopoletic cell stimulation; cancer; kw bone marrow reconstitution; haematological disease; immune deficiency; drug-induced myelosuppression; renal dialysis; gene therapy; infection; wongenital metabolic disease; neurological disease; therapy; we dendritic cell production.

**None sapiens**

**WO9818923-A1.**
                                              RESULT 9
AAW69007
ID AAW6
XX AAW6
AC AAW6
XX O1-O
XX Huma
XX Huma
XX Huma
XX Grug
KW G
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Best Local S
Matches 211
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Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions contains amino acid substitutions at positions 8, 84, 118 or 122
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211; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Page 79-80; 90pp; English.
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11arity 100.0%; Pred. No. 5.9e-98;
Conservative 0; Mismatches 0; Indels 0; Gap
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This sequence represents a rearranged human flt-3 receptor agonists of CC the invention. The agonists have a modified flt-3 ligand amino acid consequence. The agonists are used to stimulate production of haematopoietic cells in vivo (e.g. in a subject about to donate blood) or for ex vivo expansion for subsequent transplantation, e.g. to reconstitute bone CC marrow after chemotherapy, disease etc., or to treat haematological confections, burns or renal dialysis. Optionally ex vivo expanded cells are transduced with a gene therapy vector for treating e.g. congenital confections, the agonists can also be used in the treatment of tumours, infections and autoimmune disease, when administered optionally with an antigen. The agonist can also be used in the production of dendritic cells for use as an immunising adjuvant for treatment disorders including acquired immune deficiency syndrome. Compared with native ligands, the convergence of the production of dendritic convergence of the production of dendritic convergence and/or better physical properties such as solubility, stability or refold efficiency. When used together with other stimulatory agents, the
Ouery Match
Best Local Similarity
Matches 209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feng Y,
Staten N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rearranged flt-3 receptor agonists and nucleic used to stimulate production of haematopoletic for treatment of haematological diseases, bone and in gene therapy
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                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 9-10; 158pp; English
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                                                                         209
 Conservative
                                                                         AA;
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               89.7%; Score 1114; DB 19; 100.0%; Pred. No. 5.1e-97;
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PR, Woulfe SL;
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 Mismatches
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                                    Length
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B Qy Вb QY 61 27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 120 146 60 86

121 147 RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH RONFSRCLELOCOPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH

206

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181

WQRTRRRTPRPGEQVPPVPSPQDLLLVEH

AAY69720 standard; Protein; 209 B

RESULT 10
AAY69720
ID AAY69
XX
AC AAY69
XX
DI OS-JU
XX
DE Matur
XX Mature wild 05-JUL-2000 type human flt-3

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RESULT 11
AAY69723
                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAY69719) or mature (this sequence) flt3-L polypeptides. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoletic propenitor cells. The flt3-L protein can be used to induce cellular cexpansion (especially in vivo) or differentiation, e.g. in the flt3-L protein can be used to induce cellular cexpansion (especially in vivo) or dendritic cells. especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, sugment, or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autolimmunity or immunosuppression). The protein can be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, small cell lung, testicular or ovarian cancer lumbons multiple musloma neurophystoma cancer acute
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Best Local S
Matches 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions contains amino acid substitutions at positions 8, 84, 118 or 122 -
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 89-90; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multiple myeloma; leukemia
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es 209; Conserv
                                                             WORTERETPERPGEQVPPVPSPQDLLLVEH
                                                                                                                                               RONFSRCLELQCOPDSSTLPPPWSPRPLEATAPTAPOPPLLLLLLLPVGLLLLAAAWCLH
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                                                                                                                              RONFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPOPPLLLLLLPVGLLLLANAWCLH
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0: Mismatches 0
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                                    .21; Length
-97;
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Query Match Best Local Matches

Similarity

89.4%;

pred. No. 1.2e 1; Mismatches

1110; No. 1

DB 21; l.2e-96;

Length

0,

0;

Conservative

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61 87

KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 146

120 206

RONFSRCLELQCOPDSSTLPPPWSPRPLEATAPTAPOPPLLLLLLLPVGLLLLAAAWCLH KTVAGSKMQGLLERVNTEIHFVTECAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL

TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL

60 86

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The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides CC which exhibits increased or decreased biological activity relative to CC the full length wild type (AAY89719) or mature (AAY89720) flt3-L CC polypeptides. This sequence represents an example of the novel flt-3 CC ligands and comprises the K84E mutant polypeptide. The flt3-L protein CC binds cell.surface tyrosine kinase receptors and regulate growth and CC differentiation of hematopoietic progenitor cells. The flt3-L protein can be used to induce cellular expansion (especially in vivo) or CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic CC cells, especially in the presence of growth factors such as interleukins, CC colony stimulating factors or protein kinases. The protein can also CC modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein means to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, complement or enterior ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute leukemia.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions contains amino acid substitutions at positions 8, 84, 118 or 122 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV; neuroprotective; antiallergic; fit3 ligand; fit3-L; wild type; allergy; cell surface tyrosine kinase receptor; hematopoletic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppression; myelodysplasia; applastic anemia; HIV infection; lymphoma; neuroblastoma; multiple myeloma; leukemia; mutein.
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  209
                                                                                                                                                                                                                                                                                                                                                                                             84-85;
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                                                                                                                                                                                                                                                                                                                                                                                         90pp; English
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RESULT 12
AAY69726
ID AAY69
XX AAY69
XX AAY69
XX AAY69
XX AAY69
XX Immun
KW Immun
KW Immun
KW Cancle
KW Call
KW Call
XX Homo
OS Synth
XX Homo
OS OS Goliffe
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XX

The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides CC which exhibits increased or decreased biological activity relative to CC the full length wild type (Ax469719) or mature (Ax469720) flt3-L

CC polypeptides. This sequence represents an example of the novel flt-3

CC ligands and comprises the 0122R mutant polypeptide. The flt3-L protein CC binds cell surface tyrosine kinase receptors and regulate growth and CC differentiation of hematopoietic progenitor cells. The flt3-L protein CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, CC condulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, CC small cell lung, testicular or ovarian cancer, lymphoma, multiple cc myeloma, neuroblastoma or acute leukemia.
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Matches 208;
                             Query Match
Best Local
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            h 89.4%;
Similarity 99.5%;
08; Conservative
                                                                            209 AA;
        Score 1110; DB 2:
Pred. No. 1.2e-96;
1; Mismatches (
                           DB 21; Length
2e-96;
. 0; Indels . 0;
                           h 209;
      Gaps
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27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 86

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RESULT 13
AAY69727
ID Inmun
IM IMMU
IM
The invention relates to novel soluble fit3 ligand (fit3-L) polypeptides C which exhibits increased or decreased biological activity relative to the full length wild type (AAX69719) or mature (AAX69720) fit3-L CC polypeptides. This sequence represents an example of the novel fit-3 CC ligands and comprises the L26F mutant polypeptide. The fit3-L protein CC binds cell surface tyrosine kinase receptors and regulate growth and CC differentiation of hematopoietic progenitor cells. The fit3-L protein can be used to induce cellular expansion (especially in vivo) or CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, CC colony stimulating factors or protein kihases. The protein can also CC modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant soluble flt3 ligand polypeptide used in cellular expansion, immune response stimulation or treatment of pathological conditions contains amino acid substitutions at positions 8, 84, 118 or 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Page 82-83; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunity; immunosuppregsion; myelodysplasaia; applastic anemia, HIV infection; lymphoma; neuroblastoma; multiple myeloma; leukemia; mutein.
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RESULT
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The invention relates to novel soluble flt3 ligand (flt3-L) polypeptid which exhibits increased or decreased biological activity relative to the full length wild type (Aax69719) or mature (AAx697920) £lt3-L polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the L26F mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoletic progenitor cells. The flt3-L protein
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                                                                                                                                                                                                            Claim 13; Page 78-79; 90pp; English.
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Pred. Nc. 1.2e-96;
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Mutant soluble flt3 ligand polypeptide used immune response stimulation or treatment of

WPI; 2000-182115/16

02-JUL-1998;

98US-0109100 99WO-US14296

25-JUN-1999;

WO200001823-A2 Synthetic Homo sapiens

(IMMV) IMMUNEX CORP

contains amino acid substitutions

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positions

in cellular expansion, pathological condition ons 8, 84, 118 or 122

conditions

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RESULT 15
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Best Local S
Matches 208
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                                                                                                                                                                                                                                                                                                       cell surface tyrosine kinase receptor; hematopoletic progenitor cell; cellular expansion; cellular differentiation; natural killer cell; cancer; dendritic cell; immune response; autoimmunty; immunosuppression; myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY69722 standard;
                                                                                                                                                                                                                                                                                              multiple
                                                                                                                                                                                                                                                                                                                                                          Immunomodulator; immunosuppressive; cytostatic; antianemic; an neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type;
                                                                                                                                                                                                                                                                                                                                                                                                      Human
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                                                                                                                                                                                                                                                                                            leukemia;
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밁 밁 δÃ 밁 ·δ 밁 Query Match 89.2%; Best Local Similarity 99.5%; Matches 208; Conservative be used to induce cellular expansion (especially, in vivo) or differentiation, e.g. in hematopoletic, natural killer (NK) or dendritic cells, especially in the presence of growth factors such as interleukins, colony stimulating factors or protein kinases. The protein can also modulate, augment or enhance a patient's immune response and can be used to treat an immune disorder (e.g. allergy, autoimmunity or immunosuppression). The protein may be used to treat a pathological condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast, small cell lung, testicular or ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute leukemia. Sequence polypeptides. This sequence represents an example of the novel flt-3 ligands and comprises the H8Y mutant polypeptide. The flt3-L protein binds cell surface tyrosine kinase receptors and regulate growth and differentiation of hematopoletic progenitor cells. The flt3-L protein can The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides which exhibits increased or decreased biological activity relative to the full length wild type (AAX69719) or mature (AAX69720) flt3-L Claim 4; Page 81-82; 90pp; English. 207 WQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235 27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 86-61 87 KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKEWIT 120 KTVAGSKMOGLLERVNTEIHEVTKCAFOPPPSCÜREVOTNISKLIQETSBOLVALKEWIT 146 209 AA; Score 1108; DI Pred. No. 1.9e 1; Mismatches 1.9e-96; DB 21; Length 209; 0 Indels 0; Gaps 0,

Search completed: May 27, 2003, 18:27:13 Job time: 37 secs

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Database
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/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/PCT
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US-09-904-536-10
US-09-904-536-10
US-09-904-536-12
US-09-904-536-17
US-09-904-536-17
US-09-904-536-17
US-09-904-536-17
US-09-904-536-13
US-09-904-536-13
US-09-904-536-13
US-09-904-536-13
US-09-904-536-13
US-09-904-536-16
US-10-03-33554-16
US-10-03-33554-16
US-10-095-448-378-2
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10, Appl
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17, Appl
11, Appl
15, Appl
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13, Appl
16, Appl
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Sequence 56, Appl	9 US-10-001-054-56			84	4
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Sequence 50, Appl	c				Ν
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Sequence 6, Appli			7.0		w
Sequence 20, Appl	US-09-917-372-		7.0		N
Sequence 30, Appl	0S-10-174-363-30		7.1	88	ר
Sequence 2, Appl1			7.1	88.5	0
Sequence 47, Appl			7.2	89.5	9
Sequence 47, Appl	10 US-09-818-879-47		7.2	89.5	æ
Sequence 31, Appl			7.2	89.5	7
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26	US-0		7.2	89.5	Ü
Sequence 5, Appli			7.4	91.5	4
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	9 US-09-866-050A-509		7.4	91.5	N
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Sequence 19, Appl	10 US-09-904-536-19	137 1	40.8	506.5	Ö

ALIGNMENTS

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PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/669,692
FILING DATE: 24-JUN-1996
APPLICATION NUMBER: US/08/162,407
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
APPLICATION NUMBER: 08/068,394
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,449
EILING DATE: 13-Mar-2002
CLASSIFICATION: 530
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lyman, Stewart D.

Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
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LENGTH: 235
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                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 2836-D
CURRENT APPLICATION NUMBER: US/09/448,378
CURRENT FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
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                                                  181 APQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                     181 APOPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                                     121 REVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180
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LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                        235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brasel, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                       Conservative
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Pred. No. 1.4
0; Mismatches
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      181
                                          181
                                                                                                                                               Local Similarity
                                                                                                                                                                                                                              1 MTVLAPAWSPTTYLLLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
                                                                                                                                                                                                                                                                1 MTVLAPAWSPTTYLLLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version
CURRENT APPLICATION DATA:
                      APQPPLLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                               RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQFDSSTLPPPWSPRPLEATAPT
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MEDIUM TYPE: Floppy disk
      APQPPLLLLI
                                                                        RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 235 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/983,806 FILING DATE: 25-Oct-2001 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/444,626 FILING DATE: 19-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Malaska, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Stephen L. Malaska, Immunex Corporation STREET: 51 University Street
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LPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
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1.4e-101;
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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-10
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-1
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Best Local Similarity 100.0%; Pred. No. 3e
Matches 211; Conservative 0; Mismatches
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APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
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Best Local Similarity
Matches 235; Conserv
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Patent No. US20020111475Al
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TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100 PRIOR FILING DATE: 1999-07-02
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                   RLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKFW 144
                                                                                               SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWME 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APQPPLLLLLLEVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
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                                                                          SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWME 61
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RLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPW
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Pred. No. 1.4e-101;
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                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANY: Graddis, Thomas J.
APPLICANY: McGrew, Jeffrey T.
APPLICANY: MCGREW, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03200,0028
FILE REFERENCE: 03200,0028
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Best Local Similarity
Matches 209; Conserv
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SOFTWARE: PATENTIN VER. 2.1
SEQ ID NO 18
LENGTH: 209
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                                                                       SOFTWARE: PatentIn Ver.
SEQ ID NO 9
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ORGANISM: Homo sapiens
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/904,536 CURRENT FILING DATE: 2001-07-16
                                                                                                                               PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100 PRIOR FILING DATE: 1999-07-02
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PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
                                                                                                               NUMBER OF SEQ ID NOS: 20
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TYPE: PRT
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TYPE: PRT
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PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 209
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US-09-904-536-12
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                                                                    Sequence 14, Application US/09904536 Patent No. US200201111475A1 GENERAL INFORMATION:
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             APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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Patent No. US2002
CURRENT APPLICATION NUMBER: US/09/904,536
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Best Local
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CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
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ORGANISM: Homo sapiens
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US-09-904-536-17
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
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CURRENT FILING DATE: 2001-07-16
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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TYPE: PRT
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PRIOR APPLICATION NUMBER: PRIOR
PRIOR FILING DATE: 1999-07-02
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TYPE: PRT
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Pred. No. 5e-90;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-15
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                                                                                                          Best Local Similarity Matches 208; Conserv
                                                                                                                                                Query Match
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Best Local Similarity
Matches 208; Conserv
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TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
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TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 02260,0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
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PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
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EQ ID NO 11
LENGTH: 209
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Pred. No. 7.4e-90;
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Pred. No. 7.4e-90;
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US-09-904-536-13
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                  SOFTWARE: PatentIn Ver.
SEQ ID NO 8
LENGTH: 209
TYPE: PRT
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APPLICANT: Graddis, Thomas J.
APPLICANT: MCGREW, Jeffrey T.
APPLICANT: MCGREW, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
                                                                                                                                                                                                                                                                           Sequence 8, Application US/09904536 Patent No. US20020111475A1
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Best Local Similarity
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                                                                                     FILE REFERENCE: 03260.0028

CURRENT APPLICATION NUMBER: US/09/904,536

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100

PRIOR FILING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 20
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TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
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TYPE: PRT
ORGANISM: Homo sapiens
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 16
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-536-16
Search completed: May 27, 2003, 18:36:27 Job time: 58 secs
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US-09-904-536-16
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Best Local Similarity
Matches 208; Conserv
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Patent No. US20020111475A1
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Best Local Similarity 99.5
Matches 208; Conservative
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ITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
ILE REFERENCE: 03260.0028
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US-08-243-545-2
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ALIGNMENTS

SEQUENCE CHARACTERISTICS: LENGTH: 235 amino acids	
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RIECOMMINICATION INFORMATION:	
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FICATION: 435	•••
: May 24, 1993	••
APPLICATION NUMBER: 08/068 394	·. ··
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: August 12, 19	٠.
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ON: 435	•••
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CLASSIFICATION:	٠.
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APPLICATION NUMBER: US/08/243,545	٠.
LICATION DATA:	•••
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OPERATING SYSTEM: Macintosh 7.0.1	٠. ٠
PE: FL	
READABLE FORM	٠.
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STATE: Washington .	٠. ٠
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EE: Stephen L.	
DENCE ADDRESS	٠.
R OF SEQUENCES: 8	٠.
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors	•• •
Lyman, Stewar	
RMATION:	; GE
No. 5554512	; Patent
Sequence 6, Application US/08243545	; Seq

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Best Local Similarity 100.0%;
Matches 235; Conservative
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                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: December 18
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION US/O
FILING DATE: December 3
                                                                                                                                       APPLICATION NUMBER: 08
FILING DATE: August 12
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: May 24,
CLASSIFICATION: 424
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macinto:
SOFTWARE: Microsoft Word,
                                                   REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                       NAME: Malaska, Stephen L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                   TELEPHONE:
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Beckmann, M. Patricia
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                                     (206)
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                                                                                                                                                                                                                            UMBER: 08/106,463
August 12, 1993
                                                                                                     Stephen
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                                                                                                                                                                          08/068,394
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Best Local Similarity 100
Matches 235; Conservative
                                                                                    APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA: 08/106,463
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA: APPLICATION UMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version
CURRENT APPLICATION DATA:
             REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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LENGTH: 235 amino acid
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CITY: Seattle
STATE: Washing
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TELEPHONE:
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                                                                     Malaska, Stephen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09160841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 University Street
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-1
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Sequence 6, Application PC/TUS9405365 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/109,100C CURRENT FILING DATE: 1998-07-02 NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Graddis, Thomas J.
APPLICANT: MCGICW, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENERAL INFORMATION:
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                                                                                                                                                                               RFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPT 180
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                                                                                            APOPPLILLLIPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
                                                                                                                            APQPPLLLLLLPVGLLLLAAAWCLHWQRTRRRTPRPGEQVPPVPSPQDLLLVEH 235
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Pred. No. 1
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Pred. No. 1.7e-1
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1.7e-117;
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RFVQTNISRLLQETSEQLVALKPWITRQNESRCLELQCQPDSSTLPPPWSPRPLEATAPT 180

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Query Match
Best Local 9
                                                          Matches
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TELEX: 756822
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                         MOLECULE TYPE;
                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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STATE: Washington
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                    Similarity
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                                                         Conservative
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August 12, 1993
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                                                                  Score 1242; DB 5;
Pred. No. 1.7e-117;
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US-09-109-100-10
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                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
                                                         Matches
                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/09109100C Patent No. 6291661
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-1L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
LENGTH: 212
                                                                                                                                                                                                                                                         APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
                                                                                                                                                    TYPE: PRT
                                                                                                                                 ORGANISM: Homo sapiens
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27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL 86
                                                     Local Similarity
nes 209; Conserv
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ilarity 100.0%;
Conservative
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                                                               Score 1114; DB 4; Length; Pred. No. 1.2e-104;
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                            CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 209
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 02360.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 209
LENGTH: 209
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                                                                                                                                                                                                                                                            Sequence 12, Application US/09109100C Patent No. 6291661
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                                                                                                                                                          APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MU
FILE REFERENCE: 03260_0028
09-109-100-12
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TYPE: PRT
               ORGANISM: Homo sapiens
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Pred. No. 3e-104;
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US-09-109-100-14
                                                                                               GENERAL INFORMATION:
                                                                                                              Sequence 17, Appli
Patent No. 6291661
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Best Local Similarity
Matches 208; Conserv
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Patent No. 6291661
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                          APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C CURRENT FILING DATE: 1998-07-02
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 209
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
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Pred. No. 3e
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SOFTWARE: PatentIn Ver: 2
SEQ ID NO 11
SEQ ID NO 11
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo
US-09-109-100-17
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Best Local S
Matches 208
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Best Local Similarity
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SOFTWARE: PatentIn Ver. :
SEQ ID NO 17
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUT
FILE REFERENCE: 03260.0028
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               WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                    RQNESRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH
                                                                     RQNFSRCLELQCQPDSSTLPPPPWSPRPLEATAPTAPQPPLLLLLLLLPVGLLLLAAAWCLH
                                                                                                         KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 146
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WORTERETPREGEOVPPVPSPQDLLLVEH
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99.5%;
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Pred. No. 4.8e-104;
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Pred. No. 3e-104;
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RESULT 13
US-09-109-100-15
; Sequence 15, Application
; Patent No. 6291661

US/09109100C

181 WQRTRRRTPRPGEQVPPVPSPQDLLLVEH

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Matches
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 209
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APPLICANT: Graddis, Thomas J.
APPLICANT: MCGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MU
FILE REFERENCE: 03260.0028
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Best Local Similarity
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TYPE: PRT
ORGANISM: Homo sapiens
-09-109-100-13
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APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
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EQ ID NO 15
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207 WORTERFIPRPGEQVPPVPSPQDLLLVEH 235
                                                                                    147 RONFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH 205
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                                           RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLLPVGLLLLAAAWC
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                                                                                                                                                                                                                                                                                                                                                     Score 1107;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
ITILE OF INVENTION: FLIT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO8
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
Search completed: May 27, 2003, 18:28:59
Job time: 17 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09109100C Patent No. 6291661
                                                                                    181
                                                                                                                                207
                                                                                                                                                                      121 RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH
                                                                                                                                                                                                                                                     61 KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 120
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                                                                                                                                                                                                                                                                                                                                   TQDCSFQRSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGGLWRLVLAQRWMERL
                                                                                 WQRTRRRTPRPGEQVPPVPSPQDLLLVEH
                                                                                                                                                                                                                                                                                             KTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWIT 146
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                                                                                                                                                                                                             RQNFSRCLELQCQPDSSTLPPPWSPRPLEATAPTAPQPPLLLLLLLPVGLLLLAAAWCLH 206
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99.5%;
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Pred..No. 7
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